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<110> Hugh Allen Oliver Hill et al.

<120> HYDROGEN PEROXIDE OXIDATION

<130> H0-P03373US0

<160> 36

<170> PatentIn version 3.2

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 Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
 385 390 395 400
 Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
 405 410 415
 Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
 420 425 430
 Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
 435 440 445
 Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
 450 455 460
 Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn
 465 470 475 480
 Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
 485 490 495
 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
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 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
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 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
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 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
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 Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
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 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
 595 600 605
 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
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 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
 625 630 635 640
 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
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Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu
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 Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile
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 Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln
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 Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met
 755 760 765
 Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu
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 Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr
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 Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser
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 Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile
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 Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser
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 Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile
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 Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg
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 Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp
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 Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro
 995 1000 1005
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Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
20          25          30

gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt gta      144
Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
35          40          45

acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat gaa      192
Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
50          55          60

tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt gat      240
Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
65          70          75          80

ttt gca gga gac ggg tta gct aca agc tgg acg cat gaa aaa aat tgg      288
Phe Ala Gly Asp Gly Leu Ala Thr Ser Trp Thr His Glu Lys Asn Trp
85          90          95

aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca atg      336
Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
100         105         110

aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt caa      384
Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
115         120         125

aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa gac      432
Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
130         135         140

atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac tat      480
Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
145         150         155         160

cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca agt      528
Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
165         170         175

atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca aat      576
Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
180         185         190

cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa gat      624
Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
195         200         205

atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc aaa      672
Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
210         215         220

gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac gga      720
Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
225         230         235         240

aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc tat      768

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Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu			
260	265	270	
tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta caa			864
Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln			
275	280	285	
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Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser			
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Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu			
305	310	315	320
gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca aaa			1008
Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys			
325	330	335	
gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac gaa			1056
Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu			
340	345	350	
cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg gga			1104
Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly			
355	360	365	
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Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala			
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Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys			
385	390	395	400
atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt atg			1248
Ile Gly Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met			
405	410	415	
atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg gat			1296
Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp			
420	425	430	
att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa gca			1344
Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala			
435	440	445	
aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act gaa			1392
Lys Ser Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu			
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Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr			
465	470	475	480
ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga acg			1488
Pro Leu Leu Val Leu Tyr Ser Asn Met Gly Thr Ala Glu Gly Thr			
485	490	495	
gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg cag			1536
Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln			
500	505	510	
gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga gct			1584
Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala			
515	520	525	
gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac gca			1632
Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala			
530	535	540	
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Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys 545 550 555 560	
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gat gca tca cag caa atc cgt ctg gaa gca gaa gaa aaa tta gct Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Lys Leu Ala 725 730 735	2208
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Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala			
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tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc ttt		2640	
Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe			
865	870	875	880
att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa acg		2688	
Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr			
885	890	895	
ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga ggc		2736	
Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly			
900	905	910	
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Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly			
915	920	925	
gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat ctg		2832	
Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu			
930	935	940	
tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg ctt		2880	
Tyr Gln Glu Glu Leu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu			
945	950	955	960
cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt cag		2928	
His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln			
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His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln			
980	985	990	
gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct gcc		3024	
Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala			
995	1000	1005	
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Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val			
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35	40	45	
Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu			
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Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp			
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 Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
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 Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
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 Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
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 Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
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 Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
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 Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu
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 Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly
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 Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala
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 Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met
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 Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp
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 Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr
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 Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val
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 Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu
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 Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu
 675 680 685
 Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro
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 His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Leu Leu Gln Tyr
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 Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val
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 Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala
 850 855 860
 Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
 865 870 875 880
 Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr

885

890

895

Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
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 915 920 925

Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
 930 935 940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
 945 950 955 960

His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
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His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
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Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
 995 1000 1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
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 Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
 20 25 30

gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt gta 144
 Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
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 Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
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aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt caa Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln 115 120 125	384
aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa gac Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp 130 135 140	432
atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac tat Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr 145 150 155 160	480
cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca agt Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser 165 170 175	528
atg gtc cgt gca ctg gat gaa gca atg aac aag cag cag cga gca aat Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Gln Gln Arg Ala Asn 180 185 190	576
cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa gat Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp 195 200 205	624
atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc aaa Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys 210 215 220	672
gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac gga Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly 225 230 235 240	720
aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc tat Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr 245 250 255	768
caa att att aca ttc tta att gcg gga cac gaa aca aca agt ggt ctt Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu 260 265 270	816
tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta caa Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln 275 280 285	864
aaa gca gca gaa gaa gca gca cga gtt cta gta gat cct gtt cca agc Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser 290 295 300	912
tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac gaa Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu 305 310 315 320	960
gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca aaa Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys 325 330 335	1008
gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac gaa Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu 340 345 350	1056
cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg gga Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly 355 360 365	1104
gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt gcg Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala 370 375 380	1152
att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg tgt Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys 385 390 395 400	1200
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aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act gaa Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu 450 455 460	1392
cag tct gct aaa aaa gta cgc aaa aag gca gaa aac gct cat aat acg Gln Ser Ala Lys Lys Val Arg Lys Ala Glu Asn Ala His Asn Thr 465 470 475 480	1440
ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga acg Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr 485 490 495	1488
gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg cag Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln 500 505 510	1536
gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga gct Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala 515 520 525	1584
gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac gca Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala 530 535 540	1632
aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta aaa Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys 545 550 555 560	1680
ggc gtt cgc tac tcc gta ttt gga tgc ggc gat aaa aac tgg gct act Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr 565 570 575	1728
acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct aaa Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys 580 585 590	1776
ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac gac Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp 595 600 605	1824
ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac gta Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val 610 615 620	1872
gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa tct Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser 625 630 635 640	1920
act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt gcg Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala 645 650 655	1968
aaa atg cac ggt gcg ttt tca acg aac gtc gta gca agc aaa gaa ctt Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu 660 665 670	2016
caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa ctt Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu 675 680 685	2064
cca aaa gaa gct tct tat caa gaa gga gat cat tta ggt gtt att cct Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro 690 695 700	2112
cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc cta Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu 705 710 715 720	2160

gat gca tca cag caa atc cgt ctg gaa gca gaa gaa aaa tta gct Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala	725	730	735	2208
cat ttg cca ctc gct aaa aca gta tcc gta gaa gag ctt ctg caa tac His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr	740	745	750	2256
gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg gct Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala	755	760	765	2304
gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg ctt Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu	770	775	780	2352
gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca atg Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met	785	790	795	800
ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc gaa Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu	805	810	815	2448
ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att tct Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser	820	825	830	2496
tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc gtt Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val	835	840	845	2544
gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att gcg Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala	850	855	860	2592
tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc ttt Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe	865	870	875	880
att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa acg Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr	885	890	895	2688
ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga ggc Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly	900	905	910	2736
ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt gga Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly	915	920	925	2784
gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat ctg Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu	930	935	940	2832
tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg ctt Tyr Gln Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu	945	950	955	960
cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt cag His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln	965	970	975	2928
cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat caa His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln	980	985	990	2976
gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct gcc Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala	995	1000	1005	3024
gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val	1010	1015	1020	3069

agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa	3114
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys	
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ggc cga tac gca aaa gac gtg tgg gct ggg taa	3147
Gly Arg Tyr Ala Lys Asp Val Trp Ala Gly	
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Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val	
35 40 45	
Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu	
50 55 60	
Ser Arg Phe Asp Lys Asn Leu Ser Gln Gly Leu Lys Phe Val Arg Asp	
65 70 75 80	
Phe Ala Gly Asp Gly Leu Val Thr Ser Trp Thr His Glu Lys Asn Trp	
85 90 95	
Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met	
100 105 110	
Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln	
115 120 125	
Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp	
130 135 140	
Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr	
145 150 155 160	
Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser	
165 170 175	
Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Gln Gln Arg Ala Asn	
180 185 190	
Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp	
195 200 205	
Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys	
210 215 220	
Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly	
225 230 235 240	
Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr	
245 250 255	
Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu	
260 265 270	
)	
Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln	
275 280 285	
Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser	
290 295 300	

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu
 305 310 315 320

Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys
 325 330 335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu
 340 345 350

Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly
 355 360 365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala
 370 375 380

Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys
 385 390 395 400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met
 405 410 415

Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp
 420 425 430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala
 435 440 445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu
 450 455 460

Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr
 465 470 475 480

Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr
 485 490 495

Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln
 500 505 510

Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala
 515 520 525

Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala
 530 535 540

Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys
 545 550 555 560

Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr
 565 570 575

Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys
 580 585 590

Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp
 595 600 605

Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val
 610 615 620

Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser
 625 630 635 640

Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala
 645 650 655

Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu
 660 665 670

Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu
 675 680 685

Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro
 690 695 700

Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu
 705 710 715 720

Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala
 725 730 735

His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr
 740 745 750

Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala
 755 760 765

Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu
 770 775 780

Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met
 785 790 795 800

Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu
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Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser
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Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val
 835 840 845

Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala
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Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
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Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
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Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
 900 905 910

Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly
 915 920 925

Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
 930 935 940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
 945 950 955 960

His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
 965 970 975

His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
 980 985 990

Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
 995 1000 1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
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Arg Thr Phe Thr Trp Phe Thr Pro Ala Arg Arg Lys Pro Thr Glu Tyr
20 25 30

gag ctc tac acc gtg ggt caa cag tcc act ccg gac gag tgg ctg cat 144
Glu Leu Tyr Thr Val Gly Gln Ser Thr Pro Asp Glu Trp Leu His
35 40 45

gtg gac tgg ccg ctg cgc ttc gac gac ggc cgc gcc ccg tgg gag gag 192
Val Asp Trp Pro Leu Arg Phe Asp Asp Gly Arg Ala Pro Trp Glu Glu
50 55 60

gag tcg agt gcg gta cgg acc tcg gag tgg tcg gct tac cgc gac cca 240
Glu Ser Ser Ala Val Arg Thr Ser Glu Trp Ser Ala Tyr Arg Asp Pro
65 70 75 80

cac caa ctg tgg cag cgt ccc tac gtc agc acg tgc aac cag gac cag 288
His Gln Leu Trp Gln Arg Pro Tyr Val Ser Thr Cys Asn Gln Asp Gln
85 90 95

cag gcc ctc gcg cgg ctg gtc ccc gtc ctg acc atg ggg tcg gcg gcg 336
Gln Ala Leu Ala Arg Leu Val Pro Val Leu Thr Met Gly Ser Ala Ala
100 105 110

atc acg ccc atc tgg tcg cag aag atc ctc gcc agg tcc tac gcc gcc 384
Ile Thr Pro Ile Trp Ser Gln Ile Leu Ala Arg Ser Tyr Ala Ala
115 120 125

tgg cca ttc gtc gag tac ggg ctc ttc ctg agc ctg gcc tac gcc gtg 432
Trp Pro Phe Val Glu Tyr Gly Leu Phe Leu Ser Leu Ala Tyr Ala Val
130 135 140

cgc cag gcc atg tcc gac acg gtc cag ttc agc gtg gtg ttc cag gcc 480
Arg Gln Ala Met Ser Asp Thr Val Gln Phe Ser Val Val Phe Gln Ala
145 150 155 160

gtg gac cgc atg cgg ctg ctc cag gac atc gtc cac cac ctg gac cac 528
Val Asp Arg Met Arg Leu Leu Gln Asp Ile Val His His Leu Asp His
165 170 175

ctg cag gag tcg ccg gaa ttc agc gac gcc ggg gcc cgc gag gcc tgg 576
Leu Gln Glu Ser Pro Glu Phe Ser Asp Ala Gly Ala Arg Glu Ala Trp
180 185 190

atg tcc gac tcc acc ctg gtc ccg atc cgg gaa gtg atc gag cgc atc 624
Met Ser Asp Ser Thr Leu Val Pro Ile Arg Glu Val Ile Glu Arg Ile
195 200 205

gcc gcc agc cag gac tgg gtg gag atc ctg gtc gcc ggc acg ctc gtc 672
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ttc gag cct ctg gtc ggc cac ctg gcg aag gcc gag ttg ttc agc cgc 720
Phe Glu Pro Leu Val Glu His Leu Ala Lys Ala Glu Leu Phe Ser Arg
225 230 235 240

cgt gcg cca atg ttc ggg gac ggg acc acg ccg gcg gtg ctg gcg tcg 768
Arg Ala Pro Met Phe Gly Asp Gly Thr Thr Pro Ala Val Leu Ala Ser
245 250 255

gcc ctg ctg gac agc ggc agg cac ctc gaa tcg gtc cag gcg ctc gtc 816
Ala Leu Leu Asp Ser Gly Arg His Leu Glu Ser Val Gln Ala Leu Val
260 265 270

cgc ctc gtc tgc caa gac ccc gtc cat ggc gac cag aac cag gcg act 864
Arg Leu Val Cys Gln Asp Pro Val His Gly Asp Gln Asn Gln Ala Thr
275 280 285

gtg cgg cgg tgg atc gag gaa tgg cag ccg cgg tgc aag gcg gcg gcc 912
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290	295	300	
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		315	320
agc gcc aac gcg ctg tcc cgg gcg ctg gcg aac cag cgg gcc gtc Ser Ala Asn Ala Leu Ser Arg Ala Leu Ala Asn Gln Arg Ala Ala Val	325	330	1008
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gag ggc gcc ggc atc acg gca tga Glu Gly Ala Gly Ile Thr Ala			1032
	340		
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Glu Leu Tyr Thr Val Gly Gln Gln Ser Thr Pro Asp Glu Trp Leu His 35 40 45			
Val Asp Trp Pro Leu Arg Phe Asp Asp Gly Arg Ala Pro Trp Glu Glu 50 55 60			
Glu Ser Ser Ala Val Arg Thr Ser Glu Trp Ser Ala Tyr Arg Asp Pro 65 70 75 80			
His Gln Leu Trp Gln Arg Pro Tyr Val Ser Thr Cys Asn Gln Asp Gln 85 90 95			
Gln Ala Leu Ala Arg Leu Val Pro Val Leu Thr Met Gly Ser Ala Ala 100 105 110			
Ile Thr Pro Ile Trp Ser Gln Lys Ile Leu Ala Arg Ser Tyr Ala Ala 115 120 125			
Trp Pro Phe Val Glu Tyr Gly Leu Phe Leu Ser Leu Ala Tyr Ala Val 130 135 140			
Arg Gln Ala Met Ser Asp Thr Val Gln Phe Ser Val Val Phe Gln Ala 145 150 155 160			
Val Asp Arg Met Arg Leu Leu Gln Asp Ile Val His His Leu Asp His 165 170 175			
Leu Gln Glu Ser Pro Glu Phe Ser Asp Ala Gly Ala Arg Glu Ala Trp 180 185 190			
Met Ser Asp Ser Thr Leu Val Pro Ile Arg Glu Val Ile Glu Arg Ile 195 200 205			
Ala Ala Ser Gln Asp Trp Val Glu Ile Leu Val Ala Gly Thr Leu Val 210 215 220			
Phe Glu Pro Leu Val Gly His Leu Ala Lys Ala Glu Leu Phe Ser Arg 225 230 235 240			
Arg Ala Pro Met Phe Gly Asp Gly Thr Thr Pro Ala Val Leu Ala Ser 245 250 255			
Ala Leu Leu Asp Ser Gly Arg His Leu Glu Ser Val Gln Ala Leu Val 260 265 270			
Arg Leu Val Cys Gln Asp Pro Val His Gly Asp Gln Asn Gln Ala Thr 275 280 285			

Val Arg Arg Trp Ile Glu Glu Trp Gln Pro Arg Cys Lys Ala Ala Ala
 290 295 300

Gln Ser Phe Leu Pro Thr Phe Ser Asp Cys Gly Ile Asp Ala Lys Glu
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Glu Gly Ala Gly Ile Thr Ala
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Trp Asp Phe Thr Ser Val Glu Arg Arg Pro Lys Phe Glu Thr Lys Tyr	
20 25 30	
aag atg ccc aag aag ggc aag gac ccg ttc cgc gtc ctg atc cgt gac	144
Lys Met Pro Lys Lys Gly Lys Asp Pro Phe Arg Val Leu Ile Arg Asp	
35 40 45	
tac atg aag atg gaa gcg gag aag gac gac ccg acc cat ggc ttc ctc	192
Tyr Met Lys Met Glu Ala Glu Lys Asp Asp Arg Thr His Gly Phe Leu	
50 55 60	
gac ggc gcc gtg cgg acg cgt gag gcc acc agg att gag ccg cgg ttc	240
Asp Gly Ala Val Arg Thr Arg Glu Ala Thr Arg Ile Glu Pro Arg Phe	
65 70 75 80	
gct gag gcc atg aag atc atg gtg ccg cag ctg acc aac gcc gag tac	288
Ala Glu Ala Met Lys Ile Met Val Pro Gln Leu Thr Asn Ala Glu Tyr	
85 90 95	
cag gcg gtg gcg ggc tgc gga atg atc atc tcg gcc gtc gag aac cag	336
Gln Ala Val Ala Gly Cys Gly Met Ile Ile Ser Ala Val Glu Asn Gln	
100 105 110	
gag ctc cgt cag ggc tac gcc gct cag atg ctc gat gag gtg cgg cac	384
Glu Leu Arg Gln Gly Tyr Ala Ala Gln Met Leu Asp Glu Val Arg His	
115 120 125	
gcg cag ctc gag atg acg cta cgc aac tac tac gcg aag cac tgg tgc	432
Ala Gln Leu Glu Met Thr Leu Arg Asn Tyr Tyr Ala Lys His Trp Cys	
130 135 140	
gat ccc tcc ggc ttc gac atc ggt cag cgc ggc ctg tac cag cac ccc	480
Asp Pro Ser Gly Phe Asp Ile Gly Gln Arg Gly Leu Tyr Gln His Pro	
145 150 155 160	
gcg ggg ctg gtg tcc atc ggc gag ttc cag cac ttc aat act ggt gac	528
Ala Gly Leu Val Ser Ile Gly Glu Phe Gln His Phe Asn Thr Gly Asp	
165 170 175	
ccg ctt gac gtc atc atc gat ctc aac atc gtg gcc gag acg gcg ttc	576
Pro Leu Asp Val Ile Ile Asp Leu Asn Ile Val Ala Glu Thr Ala Phe	
180 185 190	
acg aac atc ctg ctg gtg gcc act cca cag gtc gcc gtg gcc aac ggg	624
Thr Asn Ile Leu Leu Val Ala Thr Pro Gln Val Ala Val Ala Asn Gly	
195 200 205	

gac aac gcg atg gcc agc gtg ttc ctc tcg atc cag tcg gac gag gcc Asp Asn Ala Met Ala Ser Val Phe Leu Ser Ile Gln Ser Asp Glu Ala 210 215 220	672
agg cac atg gcc aac ggg tac ggc tcg gtc atg gcg ctg ctg gag aac Arg His Met Ala Asn Gly Tyr Gly Ser Val Met Ala Leu Leu Glu Asn 225 230 235 240	720
gag gac aac ctc ccg ctg ctc aac cag tct ctc gat cgg cac ttc tgg Glu Asp Asn Leu Pro Leu Leu Asn Gln Ser Leu Asp Arg His Phe Trp 245 250 255	768
cgt gcc cac aag gcc ttg gac aac gcg gtc gga tgg tgt tcg gag tat Arg Ala His Lys Ala Leu Asp Asn Ala Val Gly Trp Cys Ser Glu Tyr 260 265 270	816
ggc gcc cgc aag cgg cca tgg agc tac aag gcc cag tgg gag gaa tgg Gly Ala Arg Lys Arg Pro Trp Ser Tyr Lys Ala Gln Trp Glu Glu Trp 275 280 285	864
gtc gtc gac gac ttc gtg ggc ggc tac atc gac cga ctc agc gag ttc Val Val Asp Asp Phe Val Gly Gly Tyr Ile Asp Arg Leu Ser Glu Phe 290 295 300	912
ggc gtt cag gct ccg gcc tgc ctt ggc gcg gcc gac gag gtc aag Gly Val Gln Ala Pro Ala Cys Leu Gly Ala Ala Asp Glu Val Lys 305 310 315 320	960
tgg tcg cac cac acg ctc ggt cag qtg ctg tcg qcg qtg tgg ccg ctg Trp Ser His His Thr Leu Gly Gln Val Leu Ser Ala Val Trp Pro Leu 325 330 335	1008
aac ttc tgg cgc tcg gac gcc atg gga ccg gcg gac ttc gag tgg ttc Asn Phe Trp Arg Ser Asp Ala Met Gly Pro Ala Asp Phe Glu Trp Phe 340 345 350	1056
gag aac cac tac ccg ggc tgg agc gcg gcc tac cag ggt tac tgg gag Glu Asn His Tyr Pro Gly Trp Ser Ala Ala Tyr Gln Gly Tyr Trp Glu 355 360 365	1104
ggc tac aag gcg ctc gcc gac cca gca ggc gga cgc atc atg ctc cag Gly Tyr Lys Ala Leu Ala Asp Pro Ala Gly Gly Arg Ile Met Leu Gln 370 375 380	1152
gag ctg ccg ggt ctg ccg ccg atg tgt cag gtg tgc cag gtg ccg tgc Glu Leu Pro Gly Leu Pro Pro Met Cys Gln Val Cys Gln Val Pro Cys 385 390 395 400	1200
gtg atg ccg cgg ctg gat atg aac gcc gcg cgg atc atc gag ttc gag Val Met Pro Arg Leu Asp Met Asn Ala Ala Arg Ile Ile Glu Phe Glu 405 410 415	1248
ggg cag aaa atc gcg ctg tgc agc gaa ccc tgc cag cgg atc ttc acc Gly Gln Lys Ile Ala Leu Cys Ser Glu Pro Cys Gln Arg Ile Phe Thr 420 425 430	1296
aac tgg ccg gag gcg tac cgc cac cgc aag caa tac tgg gcc cgc tac Asn Trp Pro Glu Ala Tyr Arg His Arg Lys Gln Tyr Trp Ala Arg Tyr 435 440 445	1344
cac gga tgg gac ctg gcg gac gtc atc gtt gat ctc ggc tac atc cgc His Gly Trp Asp Leu Ala Asp Val Ile Val Asp Leu Gly Tyr Ile Arg 450 455 460	1392
ccg gac ggc aag acc ctc atc ggc cag ccg ctg ctc gag atg gag cgg Pro Asp Gly Lys Thr Leu Ile Gly Gln Pro Leu Leu Glu Met Glu Arg 465 470 475 480	1440
ctg tgg acc atc gac gac atc cgg gcc ctt cag tac gaa gtc aag gac Leu Trp Thr Ile Asp Asp Ile Arg Ala Leu Gln Tyr Glu Val Lys Asp 485 490 495	1488
ccg ttg cag gag gcg tga Pro Leu Gln Glu Ala 500	1506

<210> 12
 <211> 501
 <212> PRT
 <213> Nocardia corallina

 <400> 12

 Met Ala Ser Asn Pro Thr Gln Leu His Glu Lys Ser Lys Ser Tyr Asp
 1 5 10 15

 Trp Asp Phe Thr Ser Val Glu Arg Arg Pro Lys Phe Glu Thr Lys Tyr
 20 25 30

 Lys Met Pro Lys Lys Gly Lys Asp Pro Phe Arg Val Leu Ile Arg Asp
 35 40 45

 Tyr Met Lys Met Glu Ala Glu Lys Asp Asp Arg Thr His Gly Phe Leu
 50 55 60

 Asp Gly Ala Val Arg Thr Arg Glu Ala Thr Arg Ile Glu Pro Arg Phe
 65 70 75 80

 Ala Glu Ala Met Lys Ile Met Val Pro Gln Leu Thr Asn Ala Glu Tyr
 85 90 95

 Gln Ala Val Ala Gly Cys Gly Met Ile Ile Ser Ala Val Glu Asn Gln
 100 105 110

 Glu Leu Arg Gln Gly Tyr Ala Ala Gln Met Leu Asp Glu Val Arg His
 115 120 125

 Ala Gln Leu Glu Met Thr Leu Arg Asn Tyr Tyr Ala Lys His Trp Cys
 130 135 140

 Asp Pro Ser Gly Phe Asp Ile Gly Gln Arg Gly Leu Tyr Gln His Pro
 145 150 155 160

 Ala Gly Leu Val Ser Ile Gly Glu Phe Gln His Phe Asn Thr Gly Asp
 165 170 175

 Pro Leu Asp Val Ile Ile Asp Leu Asn Ile Val Ala Glu Thr Ala Phe
 180 185 190

 Thr Asn Ile Leu Leu Val Ala Thr Pro Gln Val Ala Val Ala Asn Gly
 195 200 205

 Asp Asn Ala Met Ala Ser Val Phe Leu Ser Ile Gln Ser Asp Glu Ala
 210 215 220

 Arg His Met Ala Asn Gly Tyr Gly Ser Val Met Ala Leu Leu Glu Asn
 225 230 235 240

 Glu Asp Asn Leu Pro Leu Leu Asn Gln Ser Leu Asp Arg His Phe Trp
 245 250 255

 Arg Ala His Lys Ala Leu Asp Asn Ala Val Gly Trp Cys Ser Glu Tyr
 260 265 270

 Gly Ala Arg Lys Arg Pro Trp Ser Tyr Lys Ala Gln Trp Glu Glu Trp
 275 280 285

 Val Val Asp Asp Phe Val Gly Gly Tyr Ile Asp Arg Leu Ser Glu Phe
 290 295 300

 Gly Val Gln Ala Pro Ala Cys Leu Gly Ala Ala Ala Asp Glu Val Lys
 305 310 315 320

 Trp Ser His His Thr Leu Gly Gln Val Leu Ser Ala Val Trp Pro Leu
 325 330 335

 Asn Phe Trp Arg Ser Asp Ala Met Gly Pro Ala Asp Phe Glu Trp Phe
 340 345 350

 Glu Asn His Tyr Pro Gly Trp Ser Ala Ala Tyr Gln Gly Tyr Trp Glu
 355 360 365

Gly Tyr Lys Ala Leu Ala Asp Pro Ala Gly Gly Arg Ile Met Leu Gln
 370 375 380

 Glu Leu Pro Gly Leu Pro Pro Met Cys Gln Val Cys Gln Val Pro Cys
 385 390 395 400

 Val Met Pro Arg Leu Asp Met Asn Ala Ala Arg Ile Ile Glu Phe Glu
 405 410 415

 Gly Gln Lys Ile Ala Leu Cys Ser Glu Pro Cys Gln Arg Ile Phe Thr
 420 425 430

 Asn Trp Pro Glu Ala Tyr Arg His Arg Lys Gln Tyr Trp Ala Arg Tyr
 435 440 445

 His Gly Trp Asp Leu Ala Asp Val Ile Val Asp Leu Gly Tyr Ile Arg
 450 455 460

 Pro Asp Gly Lys Thr Leu Ile Gly Gln Pro Leu Leu Glu Met Glu Arg
 465 470 475 480

 Leu Trp Thr Ile Asp Asp Ile Arg Ala Leu Gln Tyr Glu Val Lys Asp
 485 490 495

 Pro Leu Gln Glu Ala
 500

<210> 13
 <211> 1494
 <212> DNA
 <213> Xanthobacteria sp.

<220>
 <221> CDS
 <222> (1) .. (1494)

 <400> 13
 atg gcg ctc ttg aat cgg gac gat tgg tac gac atc gcg cgc gat gtc 48
 Met Ala Leu Leu Asn Arg Asp Asp Trp Tyr Asp Ile Ala Arg Asp Val
 1 5 10 15

 gac tgg acg ctc agc tat gtc gac cgc gcg gtc gcc ttt ccc gag gag 96
 Asp Trp Thr Leu Ser Tyr Val Asp Arg Ala Val Ala Phe Pro Glu Glu
 20 25 30

 tgg aaa ggc gaa aag gac att tgc ggc acg gcc tgg gac gat tgg gac 144
 Trp Lys Gly Glu Lys Asp Ile Cys Gly Thr Ala Trp Asp Asp Trp Asp
 35 40 45

 gag ccc ttc cgg gtc tcc ttc cgc gaa tat gtg atg gtc cag cgc gac 192
 Glu Pro Phe Arg Val Ser Phe Arg Glu Tyr Val Met Val Gln Arg Asp
 50 55 60

 aag gaa gcg agc gtc ggc gcc atc cgc gag gcc atg gtc cgc gcc aag 240
 Lys Glu Ala Ser Val Gly Ala Ile Arg Glu Ala Met Val Arg Ala Lys
 65 70 75 80

 gcc tat gag aag ctc gac gac ggc cac aag gcc acc tcg cac ctg cac 288
 Ala Tyr Glu Lys Leu Asp Asp Gly His Lys Ala Thr Ser His Leu His
 85 90 95

 atg ggc acc atc acc atg gtg gag cac atg gcg gtc acc atg cag agc 336
 Met Gly Thr Ile Thr Met Val Glu His Met Ala Val Thr Met Gln Ser
 100 105 110

 cgg ttc gtg cgc ttc gcg ccg tcc gcc cgc tgg cgc agc ctc ggg gcg 384
 Arg Phe Val Arg Phe Ala Pro Ser Ala Arg Trp Arg Ser Leu Gly Ala
 115 120 125

 ttc ggc atg ctg gac gag acc cgc cac acc cag ctc gac ctg cgc ttc 432
 Phe Gly Met Leu Asp Glu Thr Arg His Thr Gln Leu Asp Leu Arg Phe
 130 135 140

agc cac gat ctg ctc aac gat tcc ccg agc ttc gac tgg agc cag cgg Ser His Asp Leu Leu Asn Asp Ser Pro Ser Phe Asp Trp Ser Gln Arg	145	150	155	160	480
gcg ttc cac acc gac gaa tgg gcg gtt ctc gcc acc cgc aac ctg ttc Ala Phe His Thr Asp Glu Trp Ala Val Leu Ala Thr Arg Asn Leu Phe		165	170	175	528
gac gac atc atg ctc aac gcc gac tgc gtg gag gcg gcg ctc gcc acc Asp Asp Ile Met Leu Asn Ala Asp Cys Val Glu Ala Ala Leu Ala Thr		180	185	190	576
agc ctg acg ctg gag cac ggc ttc acc aac atc cag ttc gtg gcg ctc Ser Leu Thr Leu Glu His Gly Phe Thr Asn Ile Gln Phe Val Ala Leu		195	200	205	624
gcc tcc gac gcc atg gaa gcc ggc gac gtg aac ttc tcc aac ctc ttg Ala Ser Asp Ala Met Glu Ala Gly Asp Val Asn Phe Ser Asn Leu Leu		210	215	220	672
tgc agc atc cag acc gac gag gcg cgg cac gcc cag ttg ggc ttt ccc Ser Ser Ile Gln Thr Asp Glu Ala Arg His Ala Gln Leu Gly Phe Pro		225	230	235	720
acc ctc gac gtg atg atg aag cac gac ccc aag cgc gcc cag cag atc Thr Leu Asp Val Met Met Lys His Asp Pro Lys Arg Ala Gln Gln Ile		245	250	255	768
ctg gac gtc gcc ttc tgg cgc tcc tac cgc atc ttc cag gcg gtg acc Leu Asp Val Ala Phe Trp Arg Ser Tyr Arg Ile Phe Gln Ala Val Thr		260	265	270	816
ggc gtc tcc atg gac tac tac acg ccg gtc gcc aag cgg cag atg tcg Gly Val Ser Met Asp Tyr Tyr Thr Pro Val Ala Lys Arg Gln Met Ser		275	280	285	864
ttc aag gag ttc atg ctg gag tgg atc gtc aag cat cat gag cgc atc Phe Lys Glu Phe Met Leu Glu Trp Ile Val Lys His His Glu Arg Ile		290	295	300	912
ctg cgc gac tac ggc ctc cag aag ccc tgg tac tgg gac acg ttc gag Leu Arg Asp Tyr Gly Leu Gln Lys Pro Trp Tyr Trp Asp Thr Phe Glu		305	310	315	960
aag acc ctc gat cac ggc cac cac gcg ctg cac atc ggc acc tgg ttc Lys Thr Leu Asp His Gly His His Ala Leu His Ile Gly Thr Trp Phe		325	330	335	1008
tgg cgc ccg acc ctg ttc tgg gat ccc aat ggc ggc gtc tcg cgc gag Trp Arg Pro Thr Leu Phe Trp Asp Pro Asn Gly Gly Val Ser Arg Glu		340	345	350	1056
gag cgg cgc tgg ctg aac cag aag tat ccg aac tgg gaa gag agc tgg Glu Arg Arg Trp Leu Asn Gln Lys Tyr Pro Asn Trp Glu Glu Ser Trp		355	360	365	1104
ggc gtc ctg tgg gac gag atc atc tcc aac atc aat gcg ggc aac att Gly Val Leu Trp Asp Glu Ile Ile Ser Asn Ile Asn Ala Gly Asn Ile		370	375	380	1152
gaa aag acc ttg ccc gag acg ctg ccg atg ctg tgc aac gtc acc aac Glu Lys Thr Leu Pro Glu Thr Leu Pro Met Leu Cys Asn Val Thr Asn		385	390	395	1200
ctg ccc atc ggc tcg cac tgg gac cgc ttc cac ctg aag ccc gag cag Leu Pro Ile Gly Ser His Trp Asp Arg Phe His Leu Lys Pro Glu Gln		405	410	415	1248
ctc gtc tac aag ggg cgg ctc tac acc ttc gac agc gac gtc tcc aag Leu Val Tyr Lys Gly Arg Leu Tyr Thr Phe Asp Ser Asp Val Ser Lys		420	425	430	1296
tgg atc ttc gag ctc gat ccg gag cgc tat gcc ggc cac acc aac gtg Trp Ile Phe Glu Leu Asp Pro Glu Arg Tyr Ala Gly His Thr Asn Val		435	440	445	1344

gtc gac cgc ttc atc ggc ggg cag atc cag ccc atg acc atc gag ggc Val Asp Arg Phe Ile Gly Gly Gln Ile Gln Pro Met Thr Ile Glu Gly	1392
450 455 460	
gtg ctc aac tgg atg ggc ctg acg ccc gaa gtc atg ggc aag gac gtg Val Leu Asn Trp Met Gly Leu Thr Pro Glu Val Met Gly Lys Asp Val	1440
465 470 475 480	
ttc aac tac cgt tgg gcc ggc gat tac gcc gag aac cgg atc gcc gcc Phe Asn Tyr Arg Trp Ala Gly Asp Tyr Ala Glu Asn Arg Ile Ala Ala	1488
485 490 495	
gag taa Glu	1494

<210> 14
<211> 497
<212> PRT
<213> Xanthobacteria sp.

<400> 14

Met Ala Leu Leu Asn Arg Asp Asp Trp Tyr Asp Ile Ala Arg Asp Val 1 5 10 15	
Asp Trp Thr Leu Ser Tyr Val Asp Arg Ala Val Ala Phe Pro Glu Glu 20 25 30	
Trp Lys Gly Glu Lys Asp Ile Cys Gly Thr Ala Trp Asp Asp Trp Asp 35 40 45	
Glu Pro Phe Arg Val Ser Phe Arg Glu Tyr Val Met Val Gln Arg Asp 50 55 60	
Lys Glu Ala Ser Val Gly Ala Ile Arg Glu Ala Met Val Arg Ala Lys 65 70 75 80	
Ala Tyr Glu Lys Leu Asp Asp Gly His Lys Ala Thr Ser His Leu His 85 90 95	
Met Gly Thr Ile Thr Met Val Glu His Met Ala Val Thr Met Gln Ser 100 105 110	
Arg Phe Val Arg Phe Ala Pro Ser Ala Arg Trp Arg Ser Leu Gly Ala 115 120 125	
Phe Gly Met Leu Asp Glu Thr Arg His Thr Gln Leu Asp Leu Arg Phe 130 135 140	
Ser His Asp Leu Leu Asn Asp Ser Pro Ser Phe Asp Trp Ser Gln Arg 145 150 155 160	
Ala Phe His Thr Asp Glu Trp Ala Val Leu Ala Thr Arg Asn Leu Phe 165 170 175	
Asp Asp Ile Met Leu Asn Ala Asp Cys Val Glu Ala Ala Leu Ala Thr 180 185 190	
Ser Leu Thr Leu Glu His Gly Phe Thr Asn Ile Gln Phe Val Ala Leu 195 200 205	
Ala Ser Asp Ala Met Glu Ala Gly Asp Val Asn Phe Ser Asn Leu Leu 215 220	210
Ser Ser Ile Gln Thr Asp Glu Ala Arg His Ala Gln Leu Gly Phe Pro 225 230 235 240	
Thr Leu Asp Val Met Met Lys His Asp Pro Lys Arg Ala Gln Gln Ile 245 250 255	
Leu Asp Val Ala Phe Trp Arg Ser Tyr Arg Ile Phe Gln Ala Val Thr 260 265 270	
Gly Val Ser Met Asp Tyr Tyr Thr Pro Val Ala Lys Arg Gln Met Ser	

275

280

285

Phe Lys Glu Phe Met Leu Glu Trp Ile Val Lys His His Glu Arg Ile
 290 295 300

Leu Arg Asp Tyr Gly Leu Gln Lys Pro Trp Tyr Trp Asp Thr Phe Glu
 305 310 315 320

Lys Thr Leu Asp His His His Ala Leu His Ile Gly Thr Trp Phe
 325 330 335

Trp Arg Pro Thr Leu Phe Trp Asp Pro Asn Gly Gly Val Ser Arg Glu
 340 345 350

Glu Arg Arg Trp Leu Asn Gln Lys Tyr Pro Asn Trp Glu Glu Ser Trp
 355 360 365

Gly Val Leu Trp Asp Glu Ile Ile Ser Asn Ile Asn Ala Gly Asn Ile
 370 375 380

Glu Lys Thr Leu Pro Glu Thr Leu Pro Met Leu Cys Asn Val Thr Asn
 385 390 395 400

Leu Pro Ile Gly Ser His Trp Asp Arg Phe His Leu Lys Pro Glu Gln
 405 410 415

Leu Val Tyr Lys Gly Arg Leu Tyr Thr Phe Asp Ser Asp Val Ser Lys
 420 425 430

Trp Ile Phe Glu Leu Asp Pro Glu Arg Tyr Ala Gly His Thr Asn Val
 435 440 445

Val Asp Arg Phe Ile Gly Gly Gln Ile Gln Pro Met Thr Ile Glu Gly
 450 455 460

Val Leu Asn Trp Met Gly Leu Thr Pro Glu Val Met Gly Lys Asp Val
 465 470 475 480

Phe Asn Tyr Arg Trp Ala Gly Asp Tyr Ala Glu Asn Arg Ile Ala Ala
 485 490 495

Glu

<210> 15

<211> 1026

<212> DNA

<213> Xanthobacteria sp.

<220>

<221> CDS

<222> (1) .. (1026)

<400> 15

atg aca cag cag cgc ccc acc cgc acg cgc gag cgc aag aag acc tgg 48
 Met Thr Gln Gln Arg Pro Thr Arg Thr Arg Glu Arg Lys Lys Thr Trp
 1 5 10 15

acg gct ttc ggc aat ctc gga cgc aag ccg acc gac tac gag gtc gtc 96
 Thr Ala Phe Gly Asn Leu Gly Arg Lys Pro Thr Asp Tyr Glu Val Val
 20 25 30

acc cac aac atg aac cac acc atg cgc ggc acg ccc ctg gag ctg tcg 144
 Thr His Asn Met Asn His Thr Met Arg Gly Thr Pro Leu Glu Leu Ser
 35 40 45

ccg acg gtg cac gcc aat gtg tgg ctc aag aag aac cgc gac gag atc 192
 Pro Thr Val His Ala Asn Val Trp Leu Lys Lys Asn Arg Asp Glu Ile
 50 55 60

gcg ctc aag gtc gac agc tgg gat ctg ttc cgc gat ccc gac cgc acc 240
 Ala Leu Lys Val Asp Ser Trp Asp Leu Phe Arg Asp Pro Asp Arg Thr
 65 70 75 80

acc tac gac acc tac gtc aag atg cag gag acc tat gtc Thr Tyr Asp Thr Tyr Val Lys Met Gln Asp Asp Gln Glu Thr Tyr Val 85 90 95	288
gac aac ctg ctc ctg tcc tac acc ggc gag ggc cgc tac gac gag gag Asp Asn Leu Leu Ser Tyr Thr Gly Glu Gly Arg Tyr Asp Glu Glu 100 105 110	336
ctt tcc tcg cgc agc ctc gac ctc ctg tcc gcg ggg ctg acg ccg acc Leu Ser Ser Arg Ser Leu Asp Leu Leu Ser Ala Gly Leu Thr Pro Thr 115 120 125	384
cgc tat ctg ggc cat ggg ctg cag atg ctc gcg gcc tat atc cag cag Arg Tyr Leu Gly His Gly Leu Gln Met Leu Ala Ala Tyr Ile Gln Gln 130 135 140	432
ctc gcc ccg tcg gcc tat gtg ggc aat tgc gcg gtg ttc cag acc tcc Leu Ala Pro Ser Ala Tyr Val Gly Asn Cys Ala Val Phe Gln Thr Ser 145 150 155 160	480
gac gcg ctg cgc cgc gtg cag cgc gtc gcc tac cgc acc cgc cag ctc Asp Ala Leu Arg Arg Val Gln Arg Val Ala Tyr Arg Thr Arg Gln Leu 165 170 175	528
gcc gac gcc cat ccg gcc cgc ggc ttc ggc tcc ggc gac cgg gcg gtg Ala Asp Ala His Pro Ala Arg Gly Phe Gly Ser Gly Asp Arg Ala Val 180 185 190	576
tgg gag aag tcc ccg gac tgg cag ccc atc cgc aag gcc atc gag gag Trp Glu Lys Ser Pro Asp Trp Gln Pro Ile Arg Lys Ala Ile Glu Glu 195 200 205	624
ctg ctc gtc acc ttc gaa tgg gac aag gcg ctc gcc ggc acc aat ttc Leu Leu Val Thr Phe Glu Trp Asp Lys Ala Leu Ala Gly Thr Asn Phe 210 215 220	672
gtg gtg aag ccg atc ctc gac gag ctg ttc ctc aac cac ctg gcg cgc Val Val Lys Pro Ile Leu Asp Glu Leu Phe Leu Asn His Leu Ala Arg 225 230 235 240	720
ctg ctc cac gtg gag ggc gac gag ctc gac agc ctc gtg ctg cgg aac Leu Leu His Val Glu Gly Asp Glu Leu Asp Ser Leu Val Leu Arg Asn 245 250 255	768
ctt cac ggc gac gcc cag cgc cac gcc cgc tgg acg gcc gcg ctc ggc Leu His Gly Asp Ala Gln Arg His Ala Arg Trp Thr Ala Ala Leu Gly 260 265 270	816
cgc ttc gcc gtc gag cag aac gtg aac aac cgc acg gtc ctg cgc gac Arg Phe Ala Val Glu Gln Asn Val Asn Asn Arg Thr Val Leu Arg Asp 275 280 285	864
gcc atc gcc ggc tgg cac gag acc ggc gag gcg gtc ctc gcc gcg ggc Ala Ile Ala Gly Trp His Glu Thr Gly Glu Ala Val Leu Ala Ala Gly 290 295 300	912
gcc ggg atg ctt gcg agc cgc gcc ccc agc gcg gat gcg gcc aag atc Ala Gly Met Leu Ala Ser Arg Ala Pro Ser Ala Asp Ala Ala Lys Ile 305 310 315 320	960
gcc gac gag gtc cgc gcc acg ctc gcg cag ctg cac gcc aat gcg ggc Ala Asp Glu Val Arg Ala Thr Leu Ala Gln Leu His Ala Asn Ala Gly 325 330 335	1008
ctc ggg cac gat gcc tga Leu Gly His Asp Ala 340	1026

<210> 16
<211> 341
<212> PRT
<213> Xanthobacteria sp.

<400> 16

Met Thr Gln Gln Arg Pro Thr Arg Thr Arg Glu Arg Lys Lys Thr Trp
 1 5 10 15

Thr Ala Phe Gly Asn Leu Gly Arg Lys Pro Thr Asp Tyr Glu Val Val
 20 25 30

Thr His Asn Met Asn His Thr Met Arg Gly Thr Pro Leu Glu Leu Ser
 35 40 45

Pro Thr Val His Ala Asn Val Trp Leu Lys Lys Asn Arg Asp Glu Ile
 50 55 60

Ala Leu Lys Val Asp Ser Trp Asp Leu Phe Arg Asp Pro Asp Arg Thr
 65 70 75 80

Thr Tyr Asp Thr Tyr Val Lys Met Gln Asp Asp Gln Glu Thr Tyr Val
 85 90 95

Asp Asn Leu Leu Ser Tyr Thr Gly Glu Gly Arg Tyr Asp Glu Glu
 100 105 110

Leu Ser Ser Arg Ser Leu Asp Leu Leu Ser Ala Gly Leu Thr Pro Thr
 115 120 125

Arg Tyr Leu Gly His Gly Leu Gln Met Leu Ala Ala Tyr Ile Gln Gln
 130 135 140

Leu Ala Pro Ser Ala Tyr Val Gly Asn Cys Ala Val Phe Gln Thr Ser
 145 150 155 160

Asp Ala Leu Arg Arg Val Gln Arg Val Ala Tyr Arg Thr Arg Gln Leu
 165 170 175

Ala Asp Ala His Pro Ala Arg Gly Phe Gly Ser Gly Asp Arg Ala Val
 180 185 190

Trp Glu Lys Ser Pro Asp Trp Gln Pro Ile Arg Lys Ala Ile Glu Glu
 195 200 205

Leu Leu Val Thr Phe Glu Trp Asp Lys Ala Leu Ala Gly Thr Asn Phe
 210 215 220

Val Val Lys Pro Ile Leu Asp Glu Leu Phe Leu Asn His Leu Ala Arg
 225 230 235 240

Leu Leu His Val Glu Gly Asp Glu Leu Asp Ser Leu Val Leu Arg Asn
 245 250 255

Leu His Gly Asp Ala Gln Arg His Ala Arg Trp Thr Ala Ala Leu Gly
 260 265 270

Arg Phe Ala Val Glu Gln Asn Val Asn Asn Arg Thr Val Leu Arg Asp
 275 280 285

Ala Ile Ala Gly Trp His Glu Thr Gly Glu Ala Val Leu Ala Ala Gly
 290 295 300

Ala Gly Met Leu Ala Ser Arg Ala Pro Ser Ala Asp Ala Ala Lys Ile
 305 310 315 320

Ala Asp Glu Val Arg Ala Thr Leu Ala Gln Leu His Ala Asn Ala Gly
 325 330 335

Leu Gly His Asp Ala
 340

<210> 17
 <211> 267
 <212> DNA
 <213> Xanthobacteria sp.

<220>
 <221> CDS
 <222> (1)...(267)

<400> 17
atg tct ttg ttc ccc atc gtg ggc cgc ttc gtg ggg gat ttc gtc ccc 48
Met Ser Leu Phe Pro Ile Val Gly Arg Phe Val Gly Asp Phe Val Pro
1 5 10 15

cac ctg gtg gcg gtg gac acc tct gac acc atc gat cag atc gcc gag 96
His Leu Val Ala Val Asp Thr Ser Asp Thr Ile Asp Gln Ile Ala Glu
20 25 30

aag gtg gcg gtc cac acg gtc ggg cgg cgc ttg ccg ccc gat ccc acc 144
Lys Val Ala Val His Thr Val Gly Arg Arg Leu Pro Pro Asp Pro Thr
35 40 45

gcc acc ggc tat gag gtg ctc ctc gac ggc gag acc ctg gac ggg ggc 192
Ala Thr Gly Tyr Glu Val Leu Leu Asp Gly Glu Thr Leu Asp Gly Gly
50 55 60

gcc acc ctg gag gcc atc atg acc aag cgc gag atg ctg ccc ctg cag 240
Ala Thr Leu Glu Ala Ile Met Thr Lys Arg Glu Met Leu Pro Leu Gln
65 70 75 80

tgg ttc gac gtg agg ttc aag aag tga 267
Trp Phe Asp Val Arg Phe Lys Lys
85

<210> 18
<211> 88
<212> PRT
<213> Xanthobacta sp.

<400> 18
Met Ser Leu Phe Pro Ile Val Gly Arg Phe Val Gly Asp Phe Val Pro
1 5 10 15

His Leu Val Ala Val Asp Thr Ser Asp Thr Ile Asp Gln Ile Ala Glu
20 25 30

Lys Val Ala Val His Thr Val Gly Arg Arg Leu Pro Pro Asp Pro Thr
35 40 45

Ala Thr Gly Tyr Glu Val Leu Leu Asp Gly Glu Thr Leu Asp Gly Gly
50 55 60

Ala Thr Leu Glu Ala Ile Met Thr Lys Arg Glu Met Leu Pro Leu Gln
65 70 75 80

Trp Phe Asp Val Arg Phe Lys Lys
85

<210> 19
<211> 1584
<212> DNA
<213> Methylococcus capsulatus

<220>
<221> CDS
<222> (1)..(1584)

<400> 19
atg gca ctt agc acc gca acc aag gcc gcg acg gac ggc ctg gct gcc 48
Met Ala Leu Ser Thr Ala Thr Lys Ala Ala Thr Asp Ala Leu Ala Ala
1 5 10 15

aat cgg gca ccc acc agc gtg aat gca cag gaa gtg cac cgt tgg ctc 96
Asn Arg Ala Pro Thr Ser Val Asn Ala Gln Glu Val His Arg Trp Leu
20 25 30

cag agc ttc aac tgg gat ttc aag aac aac cgg acc aag tac gcc acc 144
Gln Ser Phe Asn Trp Asp Phe Lys Asn Asn Arg Thr Lys Tyr Ala Thr
35 40 45

aag tac aag atg gcg aac gag acc aag gaa cag ttc aag ctg atc gcc Lys Tyr Lys Met Ala Asn Glu Thr Lys Glu Gln Phe Lys Leu Ile Ala 50 55 60	192
aag gaa tat gcg cgc atg gag gca gtc aag gac gaa agg cag ttc ggt Lys Glu Tyr Ala Arg Met Glu Ala Val Lys Asp Glu Arg Gln Phe Gly 65 70 75 80	240
agc ctg cag gat gcg ctg acc cgc ctc aac gcc ggt gtt cgc gtt cat Ser Leu Gln Asp Ala Leu Thr Arg Leu Asn Ala Gly Val Arg Val His 85 90 95	288
ccg aag tgg aac gag acc atg aaa gtg gtt tcg aac ttc ctg gaa gtg Pro Lys Trp Asn Glu Thr Met Lys Val Val Ser Asn Phe Leu Glu Val 100 105 110	336
ggc gaa tac aac gcc atc gcc gct acc ggg atg ctg tgg gat tcc gcc Gly Glu Tyr Asn Ala Ile Ala Ala Thr Gly Met Leu Trp Asp Ser Ala 115 120 125	384
cag gcg gcg gaa cag aac ggc tat ctg gcc cag gtg ttg gat gaa Gln Ala Ala Glu Gln Lys Asn Gly Tyr Leu Ala Gln Val Leu Asp Glu 130 135 140	432
atc cgc cac acc cac cag tgt gcc tac gtc aac tac tac ttc gcg aag Ile Arg His Thr His Gln Cys Ala Tyr Val Asn Tyr Tyr Phe Ala Lys 145 150 155 160	480
aac ggc cag qac ccg ggc ggt cac aac gat gct cgc cgc acc cgt acc Asn Gly Gln Asp Pro Ala Gly His Asn Asp Ala Arg Arg Thr Arg Thr 165 170 175	528
atc ggt ccg ctg tgg aag ggc atg aag cgc gtg ttt tcc gac ggc ttc Ile Gly Pro Leu Trp Lys Gly Met Lys Arg Val Phe Ser Asp Gly Phe 180 185 190	576
att tcc ggc gac gcc gtg gaa tgc tcc ctc aac ctg cag ctg gtg ggt Ile Ser Gly Asp Ala Val Glu Cys Ser Leu Asn Leu Gln Leu Val Gly 195 200 205	624
gag gcc tgc ttc acc aat ccg ctg atc gtc gca gtg acc gaa tgg gct Glu Ala Cys Phe Thr Asn Pro Leu Ile Val Ala Val Thr Glu Trp Ala 210 215 220	672
gcc gcc aac ggc gat gaa atc acc ccg acg gtg ttc ctg tcg atc gag Ala Ala Asn Gly Asp Glu Ile Thr Pro Thr Val Phe Leu Ser Ile Glu 225 230 235 240	720
acc gac gaa ctg cgc cac atg gcc aac ggt tac cag acc gtc gtt tcc Thr Asp Glu Leu Arg His Met Ala Asn Gly Tyr Gln Thr Val Val Ser 245 250 255	768
atc gcc aac gat ccg gct tcc gcc aag tat ctc aac acg gac ctg aac Ile Ala Asn Asp Pro Ala Ser Ala Lys Tyr Leu Asn Thr Asp Leu Asn 260 265 270	816
aac gcc ttc tgg acc cag cag aag tac ttc acg ccg gtg ttg ggc atg Asn Ala Phe Trp Thr Gln Gln Lys Tyr Phe Thr Pro Val Leu Gly Met 275 280 285	864
ctg ttc gag tat ggc tcc aag ttc aag gtc gag ccg tgg gtc aag acg Leu Phe Glu Tyr Gly Ser Lys Phe Lys Val Glu Pro Trp Val Lys Thr 290 295 300	912
tgg gac cgc tgg gtg tac gag gac tgg ggc ggc atc tgg atc ggc cgt Trp Asp Arg Trp Val Tyr Glu Asp Trp Gly Gly Ile Trp Ile Gly Arg 305 310 315 320	960
ctg ggc aag tac ggg gtg gag tcg ccg cgc agc ctc aag gac gcc aag Leu Gly Lys Tyr Gly Val Glu Ser Pro Arg Ser Leu Lys Asp Ala Lys 325 330 335	1008
cag gac gct tac tgg gct cac cac gac ctg tat ctg ctg gct tat gcg Gln Asp Ala Tyr Trp Ala His His Asp Leu Tyr Leu Leu Ala Tyr Ala 340 345 350	1056

ctg tgg ccg acc ggc ttc ttc cgt ctg gcg ctg ccg gat cag gaa gaa Leu Trp Pro Thr Gly Phe Phe Arg Leu Ala Leu Pro Asp Gln Glu Glu 355 360 365	1104
atg gag tgg ttc gag gcc aac tac ccc ggc tgg tac gac cac tac ggc Met Glu Trp Phe Glu Ala Asn Tyr Pro Gly Trp Tyr Asp His Tyr Gly 370 375 380	1152
aag atc tac gag gaa tgg cgc gcc cgc ggt tgc gag gat ccg tcc tcg Lys Ile Tyr Glu Glu Trp Arg Ala Arg Gly Cys Glu Asp Pro Ser Ser 385 390 395 400	1200
ggc ttc atc ccg ctg atg tgg ttc atc gaa aac aac cat ccc atc tac Gly Phe Ile Pro Leu Met Trp Phe Ile Glu Asn Asn His Pro Ile Tyr 405 410 415	1248
atc gat cgc gtg tcg caa gtg ccg ttc tgc ccg agc ttg gcc aag ggc Ile Asp Arg Val Ser Gln Val Pro Phe Cys Pro Ser Leu Ala Lys Gly 420 425 430	1296
gcc agc acc ctg cgc gtg cac gag tac aac ggc gag atg cac acc ttc Ala Ser Thr Leu Arg Val His Glu Tyr Asn Gly Glu Met His Thr Phe 435 440 445	1344
agc gac cag tgg ggc gag cgc atg tgg ctg gcc gag ccg gag cgc tac Ser Asp Gln Trp Gly Glu Arg Met Trp Leu Ala Glu Pro Glu Arg Tyr 450 455 460	1392
gag tgc cag aac atc ttc gaa cag tac gaa gga cgc gaa ctg tcg gaa Glu Cys Gln Asn Ile Phe Glu Gln Tyr Glu Gly Arg Glu Leu Ser Glu 465 470 475 480	1440
gtg atc gcc gaa ctg cac ggg ctg cgc agt gat ggc aag acc ctg atc Val Ile Ala Glu Leu His Gly Leu Arg Ser Asp Gly Lys Thr Leu Ile 485 490 495	1488
gcc cag ccg cat gtc cgt ggc gac aag ctg tgg acg ttg gac gat atc Ala Gln Pro His Val Arg Gly Asp Lys Leu Trp Thr Leu Asp Asp Ile 500 505 510	1536
aaa cgc ctg aac tgc gtc ttc aag aac ccg gtg aag gca ttc aat tga Lys Arg Leu Asn Cys Val Phe Lys Asn Pro Val Lys Ala Phe Asn 515 520 525	1584

<210> 20
<211> 527
<212> PRT
<213> Methylococcus capsulatus

<400> 20

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Asn Arg Ala Pro Thr Ser Val Asn Ala Gln Glu Val His Arg Trp Leu 20 25 30
Gln Ser Phe Asn Trp Asp Phe Lys Asn Asn Arg Thr Lys Tyr Ala Thr 35 40 45
Lys Tyr Lys Met Ala Asn Glu Thr Lys Glu Gln Phe Lys Leu Ile Ala 50 55 60
Lys Glu Tyr Ala Arg Met Glu Ala Val Lys Asp Glu Arg Gln Phe Gly 65 70 75 80
Ser Leu Gln Asp Ala Leu Thr Arg Leu Asn Ala Gly Val Arg Val His 85 90 95
Pro Lys Trp Asn Glu Thr Met Lys Val Val Ser Asn Phe Leu Glu Val 100 105 110
Gly Glu Tyr Asn Ala Ile Ala Ala Thr Gly Met Leu Trp Asp Ser Ala 115 120 125

Gln Ala Ala Glu Gln Lys Asn Gly Tyr Leu Ala Gln Val Leu Asp Glu
 130 135 140

Ile Arg His Thr His Gln Cys Ala Tyr Val Asn Tyr Tyr Phe Ala Lys
 145 150 155 160

Asn Gly Gln Asp Pro Ala Gly His Asn Asp Ala Arg Arg Thr Arg Thr
 165 170 175

Ile Gly Pro Leu Trp Lys Gly Met Lys Arg Val Phe Ser Asp Gly Phe
 180 185 190

Ile Ser Gly Asp Ala Val Glu Cys Ser Leu Asn Leu Gln Leu Val Gly
 195 200 205

Glu Ala Cys Phe Thr Asn Pro Leu Ile Val Ala Val Thr Glu Trp Ala
 210 215 220

Ala Ala Asn Gly Asp Glu Ile Thr Pro Thr Val Phe Leu Ser Ile Glu
 225 230 235 240

Thr Asp Glu Leu Arg His Met Ala Asn Gly Tyr Gln Thr Val Val Ser
 245 250 255

Ile Ala Asn Asp Pro Ala Ser Ala Lys Tyr Leu Asn Thr Asp Leu Asn
 260 265 270

Asn Ala Phe Trp Thr Gln Gln Lys Tyr Phe Thr Pro Val Leu Gly Met
 275 280 285

Leu Phe Glu Tyr Gly Ser Lys Phe Lys Val Glu Pro Trp Val Lys Thr
 290 295 300

Trp Asp Arg Trp Val Tyr Glu Asp Trp Gly Gly Ile Trp Ile Gly Arg
 305 310 315 320

Leu Gly Lys Tyr Gly Val Glu Ser Pro Arg Ser Leu Lys Asp Ala Lys
 325 330 335

Gln Asp Ala Tyr Trp Ala His His Asp Leu Tyr Leu Leu Ala Tyr Ala
 340 345 350

Leu Trp Pro Thr Gly Phe Phe Arg Leu Ala Leu Pro Asp Gln Glu Glu
 355 360 365

Met Glu Trp Phe Glu Ala Asn Tyr Pro Gly Trp Tyr Asp His Tyr Gly
 370 375 380

Lys Ile Tyr Glu Glu Trp Arg Ala Arg Gly Cys Glu Asp Pro Ser Ser
 385 390 395 400

Gly Phe Ile Pro Leu Met Trp Phe Ile Glu Asn Asn His Pro Ile Tyr
 405 410 415

Ile Asp Arg Val Ser Gln Val Pro Phe Cys Pro Ser Leu Ala Lys Gly
 420 425 430

Ala Ser Thr Leu Arg Val His Glu Tyr Asn Gly Glu Met His Thr Phe
 435 440 445

Ser Asp Gln Trp Gly Glu Arg Met Trp Leu Ala Glu Pro Glu Arg Tyr
 450 455 460

Glu Cys Gln Asn Ile Phe Glu Gln Tyr Glu Gly Arg Glu Leu Ser Glu
 465 470 475 480

Val Ile Ala Glu Leu His Gly Leu Arg Ser Asp Gly Lys Thr Leu Ile
 485 490 495

Ala Gln Pro His Val Arg Gly Asp Lys Leu Trp Thr Leu Asp Asp Ile
 500 505 510

Lys Arg Leu Asn Cys Val Phe Lys Asn Pro Val Lys Ala Phe Asn
 515 520 525

<210> 21
<211> 1170
<212> DNA
<213> Methylococcus capsulatus

<220>
<221> CDS
<222> (1) .. (1170)

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Met	Ser	Met	Leu	Gly	Glu	Arg	Arg	Arg	Gly	Leu	Thr	Asp	Pro	Glu	Met		
1			5						10						15		
gcg	gcc	gtc	att	ttg	aag	gcg	ctt	cct	gaa	gct	ccg	ctg	gac	ggc	aac	96	
Ala	Ala	Val	Ile	Leu	Lys	Ala	Leu	Pro	Glu	Ala	Pro	Leu	Asp	Gly	Asn		
			20					25							30		
aac	aag	atg	ggt	tat	ttc	gtc	acc	ccc	cgc	tgg	aaa	cgc	ttg	acg	gaa	144	
Asn	Lys	Met	Gly	Tyr	Phe	Val	Thr	Pro	Arg	Trp	Lys	Arg	Leu	Thr	Glu		
			35				40								45		
tat	gaa	gcc	ctg	acc	gtt	tat	gcg	cag	ccc	aac	gcc	gac	tgg	atc	gcc	192	
Tyr	Glu	Ala	Leu	Thr	Val	Tyr	Ala	Gln	Pro	Asn	Ala	Asp	Trp	Ile	Ala		
			50				55								60		
ggc	ggc	ctg	gac	tgg	ggc	gac	tgg	acc	cag	aaa	ttc	cac	ggc	ggc	cgc	240	
Gly	Gly	Leu	Asp	Trp	Gly	Asp	Trp	Thr	Gln	Lys	Phe	His	Gly	Gly	Arg		
			65			70			75						80		
cct	tcc	tgg	ggc	aac	gag	acc	acg	gag	ctg	cgc	acc	gtc	gac	tgg	ttc	288	
Pro	Ser	Trp	Gly	Asn	Glu	Thr	Thr	Glu	Leu	Arg	Thr	Val	Asp	Trp	Phe		
			85					90							95		
aag	cac	cgt	gac	ccg	ctc	cgc	cgt	tgg	cat	gcg	ccg	tac	gtc	aag	gac	336	
Lys	His	Arg	Asp	Pro	Leu	Arg	Arg	Trp	His	Ala	Pro	Tyr	Val	Lys	Asp		
			100					105							110		
aag	gcc	gag	gaa	tgg	cgc	tac	acc	gac	cgc	ttc	ctg	cag	ggt	tac	tcc	384	
Lys	Ala	Glu	Glu	Trp	Arg	Tyr	Thr	Asp	Arg	Phe	Leu	Gln	Gly	Tyr	Ser		
			115				120								125		
gcc	gac	ggt	cag	atc	cg	g	cg	at	g	ac	cc	tgg	cg	g	ag	ttc	432
Ala	Asp	Gly	Gln	Ile	Arg	Ala	Met	Asn	Pro	Thr	Trp	Arg	Asp	Glu	Phe		
			130				135								140		
atc	aac	cg	tat	tgg	ggc	gcc	ttc	ctg	ttc	aac	gaa	tac	gga	ttg	ttc	480	
Ile	Asn	Arg	Tyr	Trp	Gly	Ala	Phe	Leu	Phe	Asn	Glu	Tyr	Gly	Leu	Phe		
			145				150								160		
aac	gct	cat	tcg	cag	ggc	gcc	cg	g	g	cg	tg	tg	gac	gt	acc	cg	528
Asn	Ala	His	Ser	Gln	Gly	Ala	Arg	Glu	Ala	Leu	Ser	Asp	Val	Thr	Arg		
			165						170						175		
gtc	agc	ctg	gct	ttc	tgg	ggc	ttc	gac	aag	atc	gac	atc	gcc	cag	at	576	
Val	Ser	Leu	Ala	Phe	Trp	Gly	Phe	Asp	Lys	Ile	Asp	Ile	Ala	Gln	Met		
			180					185							190		
atc	caa	ctc	gaa	cg	gg	ttc	ctc	gcc	aag	atc	gt	cc	gg	ttc	gac	624	
Ile	Gln	Leu	Glu	Arg	Gly	Phe	Leu	Ala	Lys	Ile	Val	Pro	Gly	Phe	Asp		
			195					200							205		
gag	tcc	aca	g	gt	cg	aa	g	cc	gaa	tgg	ac	aa	gg	gg	gt	tc	672
Glu	Ser	Thr	Ala	Val	Pro	Lys	Ala	Glu	Trp	Thr	Asn	Gly	Glu	Val	Tyr		
			210					215							220		
aag	agc	gcc	cgt	ctg	ggc	gt	g	aa	gg	tt	cg	tg	tg	tt	gac	720	
Lys	Ser	Ala	Arg	Leu	Ala	Val	Glu	Gly	Leu	Trp	Gln	Glu	Val	Phe	Asp		
			225					230							240		
tgg	aa	g	ag	ag	g	ct	tc	gt	ca	g	cc	gg	tt	tc	gac	768	
Trp	Asn	Glu	Ser	Ala	Phe	Ser	Val	His	Ala	Val	Tyr	Asp	Ala	Leu	Phe		
			245						250						255		
ggt	cag	ttc	gtc	cg	cg	gag	ttc	ttt	cag	cg	ct	gt	cc	cg	tc	816	

Gly Gln Phe Val Arg Arg Glu Phe Phe Gln Arg Leu Ala Pro Arg Phe
 260 265 270

ggc gac aat ctg acg cca ttc ttc atc aac cag gcc cag aca tac ttc 864
 Gly Asp Asn Leu Thr Pro Phe Phe Ile Asn Gln Ala Gln Thr Tyr Phe
 275 280 285

cag atc gcc aag cag ggc gta cag gat ctg tat tac aac tgt ctg ggt 912
 Gln Ile Ala Lys Gln Gly Val Gln Asp Leu Tyr Tyr Asn Cys Leu Gly
 290 295 300

gac gat ccg gag ttc agc gat tac aac cgt acc gtg atg cgc aac tgg 960
 Asp Asp Pro Glu Phe Ser Asp Tyr Asn Arg Thr Val Met Arg Asn Trp
 305 310 315 320

acc ggc aag tgg ctg gag ccc acg atc gcc gct ctg cgc gac ttc atg 1008
 Thr Gly Lys Trp Leu Glu Pro Thr Ile Ala Ala Leu Arg Asp Phe Met
 325 330 335

ggg ctg ttt gcg aag ctg ccg gcg ggc acc act gac aag gaa gaa atc 1056
 Gly Leu Phe Ala Lys Leu Pro Ala Gly Thr Thr Asp Lys Glu Glu Ile
 340 345 350

acc gcg tcc ctg tac cgg gtg gtc gac gac tgg atc gag gac tac gcc 1104
 Thr Ala Ser Leu Tyr Arg Val Val Asp Asp Trp Ile Glu Asp Tyr Ala
 355 360 365

agc gcg atc gac ttc aag gcg gac cgc gat cag atc gtt aaa gcg gtt 1152
 Ser Ala Ile Asp Phe Lys Ala Asp Arg Asp Gln Ile Val Lys Ala Val
 370 375 380

ctg gca gga ttg aaa taa 1170
 Leu Ala Gly Leu Lys
 385

<210> 22
 <211> 389
 <212> PRT
 <213> Methylococcus capsulatus

<400> 22

Met Ser Met Leu Gly Glu Arg Arg Gly Leu Thr Asp Pro Glu Met
 1 5 10 15

Ala Ala Val Ile Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Asn
 20 25 30

Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu
 35 40 45

Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala
 50 55 60

Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg
 65 70 75 80

Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe
 85 90 95

Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp
 100 105 110

Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser
 115 120 125

Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe
 130 135 140

Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe
 145 150 155 160

Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg
 165 170 175

Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met
 180 185 190
 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp
 195 200 205
 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr
 210 215 220
 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp
 225 230 235 240
 Trp Asn Glu Ser Ala Phe Ser Val His Ala Val Tyr Asp Ala Leu Phe
 245 250 255
 Gly Gln Phe Val Arg Arg Glu Phe Phe Gln Arg Leu Ala Pro Arg Phe
 260 265 270
 Gly Asp Asn Leu Thr Pro Phe Phe Ile Asn Gln Ala Gln Thr Tyr Phe
 275 280 285
 Gln Ile Ala Lys Gln Gly Val Gln Asp Leu Tyr Tyr Asn Cys Leu Gly
 290 295 300
 Asp Asp Pro Glu Phe Ser Asp Tyr Asn Arg Thr Val Met Arg Asn Trp
 305 310 315 320
 Thr Gly Lys Trp Leu Glu Pro Thr Ile Ala Ala Leu Arg Asp Phe Met
 325 330 335
 Gly Leu Phe Ala Lys Leu Pro Ala Gly Thr Thr Asp Lys Glu Glu Ile
 340 345 350
 Thr Ala Ser Leu Tyr Arg Val Val Asp Asp Trp Ile Glu Asp Tyr Ala
 355 360 365
 Ser Ala Ile Asp Phe Lys Ala Asp Arg Asp Gln Ile Val Lys Ala Val
 370 375 380
 Leu Ala Gly Leu Lys
 385

<210> 23
 <211> 513
 <212> DNA
 <213> Methylococcus capsulatus

<220>
 <221> CDS
 <222> (1) .. (513)

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 atg gcg aaa ctg ggt ata cac agc aac gac acc cgc gac gcc tgg gtg 48
 Met Ala Lys Leu Gly Ile His Ser Asn Asp Thr Arg Asp Ala Trp Val
 1 5 10 15

aac aag atc gcg cag ctc aac acc ctg gaa aaa gcg gcc gag atg ctg 96
 Asn Lys Ile Ala Gln Leu Asn Thr Leu Glu Lys Ala Ala Glu Met Leu
 20 25 30

aag cag ttc cgg atg gac cac acc acg ccg ttc cgc aac agc tac gaa 144
 Lys Gln Phe Arg Met Asp His Thr Thr Pro Phe Arg Asn Ser Tyr Glu
 35 40 45

ctg gac aac gac tac ctc tgg atc gag gcc aag ctc gaa gag aag gtc 192
 Leu Asp Asn Asp Tyr Leu Trp Ile Glu Ala Lys Leu Glu Glu Lys Val
 50 55 60

gcc gtc ctc aag gca cgc gcc ttc aac gag gtg gac ttc cgt cat aag 240
 Ala Val Leu Lys Ala Arg Ala Phe Asn Glu Val Asp Phe Arg His Lys
 65 70 75 80

acc gct ttc ggc gag gat gcc aag tcc gtt ctg gac ggc acc gtc gcg 288
 Thr Ala Phe Gly Glu Asp Ala Lys Ser Val Leu Asp Gly Thr Val Ala

85

90

95

aag atg aac gcg gcc aag gac aag tgg gag gcg gag aag atc cat atc 336
 Lys Met Asn Ala Ala Lys Asp Lys Trp Glu Ala Glu Lys Ile His Ile
 100 105 110

ggt ttc cgc cag gcc tac aag ccg ccg atc atg ccg gtg aac tat ttc 384
 Gly Phe Arg Gln Ala Tyr Lys Pro Pro Ile Met Pro Val Asn Tyr Phe
 115 120 125

ctg gac ggc gag cgt cag ttg ggg acc ccg ctg atg gaa ctg cgc aac 432
 Leu Asp Gly Glu Arg Gln Leu Gly Thr Arg Leu Met Glu Leu Arg Asn
 130 135 140

ctc aac tac tac gac acg ccg ctg gaa gaa ctg cgc aaa cag cgc ggt 480
 Leu Asn Tyr Tyr Asp Thr Pro Leu Glu Glu Leu Arg Lys Gln Arg Gly
 145 150 155 160

gtg cgg gtg gtg cat ctg cag tcg ccg cac tga 513
 Val Arg Val Val His Leu Gln Ser Pro His
 165 170

<210> 24
<211> 170
<212> PRT
<213> Methylococcus capsulatus

<400> 24

Met Ala Lys Leu Gly Ile His Ser Asn Asp Thr Arg Asp Ala Trp Val
 1 5 10 15

Asn Lys Ile Ala Gln Leu Asn Thr Leu Glu Lys Ala Ala Glu Met Leu
 20 25 30

Lys Gln Phe Arg Met Asp His Thr Thr Pro Phe Arg Asn Ser Tyr Glu
 35 40 45

Leu Asp Asn Asp Tyr Leu Trp Ile Glu Ala Lys Leu Glu Glu Lys Val
 50 55 60

Ala Val Leu Lys Ala Arg Ala Phe Asn Glu Val Asp Phe Arg His Lys
 65 70 75 80

Thr Ala Phe Gly Glu Asp Ala Lys Ser Val Leu Asp Gly Thr Val Ala
 85 90 95

Lys Met Asn Ala Ala Lys Asp Lys Trp Glu Ala Glu Lys Ile His Ile
 100 105 110

Gly Phe Arg Gln Ala Tyr Lys Pro Pro Ile Met Pro Val Asn Tyr Phe
 115 120 125

Leu Asp Gly Glu Arg Gln Leu Gly Thr Arg Leu Met Glu Leu Arg Asn
 130 135 140

Leu Asn Tyr Tyr Asp Thr Pro Leu Glu Glu Leu Arg Lys Gln Arg Gly
 145 150 155 160

Val Arg Val Val His Leu Gln Ser Pro His
 165 170

<210> 25
<211> 1206
<212> DNA
<213> Pseudomonas oleovorans

<220>
<221> CDS
<222> (1)...(1206)

<400> 25
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Met Leu Glu Lys His Arg Val Leu Asp Ser Ala Pro Glu Tyr Val Asp				
1	5	10	15	
aaa aag aaa tat ctc tgg ata cta tca act ttg tgg ccg gct act ccg				96
Lys Lys Lys Tyr Leu Trp Ile Leu Ser Thr Leu Trp Pro Ala Thr Pro				
20	25	30		
atg atc gga atc tgg ctt gca aat gaa act ggt tgg ggg att ttt tat				144
Met Ile Gly Ile Trp Leu Ala Asn Glu Thr Gly Trp Gly Ile Phe Tyr				
35	40	45		
ggg ctg gta ttg ctc gta tgg tac ggc gca ctt cca ttg ctt gat gcg				192
Gly Leu Val Leu Val Trp Tyr Gly Ala Leu Pro Leu Leu Asp Ala				
50	55	60		
atg ttt ggt gag gac ttt aat aat ccg cct gaa gaa gtg gtg ccg aaa				240
Met Phe Gly Glu Asp Phe Asn Asn Pro Pro Glu Glu Val Val Pro Lys				
65	70	75	80	
cta gag aag gag cgg tac tat cga gtt ttg aca tat cta aca gtt cct				288
Leu Glu Lys Glu Arg Tyr Tyr Arg Val Leu Thr Tyr Leu Thr Val Pro				
85	90	95		
atg cat tac gct gca tta att gtg tca gca tgg tgg gtc gga act cag				336
Met His Tyr Ala Ala Leu Ile Val Ser Ala Trp Trp Val Gly Thr Gln				
100	105	110		
cca atg tct tgg ctt gaa att ggt gcg ctt gcc ttg tca ctg ggt atc				384
Pro Met Ser Trp Leu Glu Ile Gly Ala Leu Ala Leu Ser Leu Gly Ile				
115	120	125		
gtg aac gga cta gcg ctc aat aca gga cac gaa ctc ggt cac aag aag				432
Val Asn Gly Leu Ala Leu Asn Thr Gly His Glu Leu Gly His Lys Lys				
130	135	140		
gag act ttt gat cgt tgg atg gcc aaa att gtg ttg gct gtc gta ggg				480
Glu Thr Phe Asp Arg Trp Met Ala Lys Ile Val Leu Ala Val Val Gly				
145	150	155	160	
tac ggt cac ttc ttt att gag cat aat aag ggt cat cac cgt gat gtc				528
Tyr Gly His Phe Ile Glu His Asn Lys Gly His His Arg Asp Val				
165	170	175		
gct aca ccg atg gat cct gca aca tcc cgg atg gga gaa agc att tat				576
Ala Thr Pro Met Asp Pro Ala Thr Ser Arg Met Gly Glu Ser Ile Tyr				
180	185	190		
aag ttt tca atc cgt gag atc cca gga gca ttt att cgt gct tgg ggg				624
Lys Phe Ser Ile Arg Glu Ile Pro Gly Ala Phe Ile Arg Ala Trp Gly				
195	200	205		
ctt gag gaa caa cgc ctt tcg cgc cgt ggc caa agc gtt tgg agt ttc				672
Leu Glu Gln Arg Leu Ser Arg Arg Gly Gln Ser Val Trp Ser Phe				
210	215	220		
gat aat gaa atc ctc caa cca atg atc atc aca gtt att ctt tac gcc				720
Asp Asn Glu Ile Leu Gln Pro Met Ile Ile Thr Val Ile Leu Tyr Ala				
225	230	235	240	
gtt ctc ctt gcc ttg ttt gga cct aag atg ctg gtg ttc ctg ccg att				768
Val Leu Leu Ala Leu Phe Gly Pro Lys Met Leu Val Phe Leu Pro Ile				
245	250	255		
caa atg gct ttc ggt tgg tgg cag ctg acc agt gcg aac tat att gaa				816
Gln Met Ala Phe Gly Trp Trp Gln Leu Thr Ser Ala Asn Tyr Ile Glu				
260	265	270		
cat tac ggc ttg ctc cgt caa aaa atg gag gac ggt cga tat gag cat				864
His Tyr Gly Leu Leu Arg Gln Lys Met Glu Asp Gly Arg Tyr Glu His				
275	280	285		
caa aag ccg cac cat tct tgg aat agt aat cac atc gtc tct aat cta				912
Gln Lys Pro His His Ser Trp Asn Ser Asn His Ile Val Ser Asn Leu				
290	295	300		
gtg ctg ttc cac ctt cag cgg cac tcg gat cac cac gcg cat cca aca				960

Val Leu Phe His Leu Gln Arg His Ser Asp His His Ala His Pro Thr			
305	310	315	320
cgt tct tat cag tca ctt cg gat ttt ccc ggc ctg ccg gct ctt ccg			1008
Arg Ser Tyr Gln Ser Leu Arg Asp Phe Pro Gly Leu Pro Ala Leu Pro			
325	330	335	
acg ggt tac cct ggt gca ttt ttg atg gcg atg att cct cag tgg ttt			1056
Thr Gly Tyr Pro Gly Ala Phe Leu Met Ala Met Ile Pro Gln Trp Phe			
340	345	350	
aga tca gtt atg gat ccc aag gta gta gat tgg gct ggt gac ctt			1104
Arg Ser Val Met Asp Pro Lys Val Val Asp Trp Ala Gly Gly Asp Leu			
355	360	365	
aat aag atc caa att gat gat tcg atg cga gaa acc tat ttg aaa aaa			1152
Asn Lys Ile Gln Ile Asp Asp Ser Met Arg Glu Thr Tyr Leu Lys Lys			
370	375	380	
ttt ggc act agt agt gct ggt cat agt tcg agt acc tct gcg gta gca			1200
Phe Gly Thr Ser Ser Ala Gly His Ser Ser Thr Ser Ala Val Ala			
385	390	395	400
tcg tag			1206
Ser			

<210> 26			
<211> 401			
<212> PRT			
<213> Pseudomonas oleovorans			
<400> 26			
Met Leu Glu Lys His Arg Val Leu Asp Ser Ala Pro Glu Tyr Val Asp			
1	5	10	15
Lys Lys Lys Tyr Leu Trp Ile Leu Ser Thr Leu Trp Pro Ala Thr Pro			
20	25	30	
Met Ile Gly Ile Trp Leu Ala Asn Glu Thr Gly Trp Gly Ile Phe Tyr			
35	40	45	
Gly Leu Val Leu Leu Val Trp Tyr Gly Ala Leu Pro Leu Leu Asp Ala			
50	55	60	
Met Phe Gly Glu Asp Phe Asn Asn Pro Pro Glu Glu Val Val Pro Lys			
65	70	75	80
Leu Glu Lys Glu Arg Tyr Tyr Arg Val Leu Thr Tyr Leu Thr Val Pro			
85	90	95	
Met His Tyr Ala Ala Leu Ile Val Ser Ala Trp Trp Val Gly Thr Gln			
100	105	110	
Pro Met Ser Trp Leu Glu Ile Gly Ala Leu Ala Leu Ser Leu Gly Ile			
115	120	125	
Val Asn Gly Leu Ala Leu Asn Thr Gly His Glu Leu Gly His Lys Lys			
130	135	140	
Glu Thr Phe Asp Arg Trp Met Ala Lys Ile Val Leu Ala Val Val Gly			
145	150	155	160
Tyr Gly His Phe Phe Ile Glu His Asn Lys Gly His His Arg Asp Val			
165	170	175	
Ala Thr Pro Met Asp Pro Ala Thr Ser Arg Met Gly Glu Ser Ile Tyr			
180	185	190	
Lys Phe Ser Ile Arg Glu Ile Pro Gly Ala Phe Ile Arg Ala Trp Gly			
195	200	205	
Leu Glu Glu Gln Arg Leu Ser Arg Arg Gly Gln Ser Val Trp Ser Phe			
210	215	220	

Asp Asn Glu Ile Leu Gln Pro Met Ile Ile Thr Val Ile Leu Tyr Ala
225 230 235 240

Val Leu Leu Ala Leu Phe Gly Pro Lys Met Leu Val Phe Leu Pro Ile
245 250 255

Gln Met Ala Phe Gly Trp Trp Gln Leu Thr Ser Ala Asn Tyr Ile Glu
260 265 270

His Tyr Gly Leu Leu Arg Gln Lys Met Glu Asp Gly Arg Tyr Glu His
275 280 285

Gln Lys Pro His His Ser Trp Asn Ser Asn His Ile Val Ser Asn Leu
290 295 300

Val Leu Phe His Leu Gln Arg His Ser Asp His His Ala His Pro Thr
305 310 315 320

Arg Ser Tyr Gln Ser Leu Arg Asp Phe Pro Gly Leu Pro Ala Leu Pro
325 330 335

Thr Gly Tyr Pro Gly Ala Phe Leu Met Ala Met Ile Pro Gln Trp Phe
340 345 350

Arg Ser Val Met Asp Pro Lys Val Val Asp Trp Ala Gly Gly Asp Leu
355 360 365

Asn Lys Ile Gln Ile Asp Asp Ser Met Arg Glu Thr Tyr Leu Lys Lys
370 375 380

Phe Gly Thr Ser Ser Ala Gly His Ser Ser Ser Thr Ser Ala Val Ala
385 390 395 400

Ser

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<210> 27
<211> 1560
<212> DNA
<213> Burkholderia cepacia

<220>
<221> CDS
<222> (1)..(1560)

<400> 27
atg gac act tct gtg cag aag aag aaa ctc ggt tta aag aat cgc tac 48
Met Asp Thr Ser Val Gln Lys Lys Lys Leu Gly Leu Lys Asn Arg Tyr
1 5 10 15

gca gcg atg acc cgc ggt ctt ggc tgg cag acc agc tac cag ccg atg 96
Ala Ala Met Thr Arg Gly Leu Gly Trp Gln Thr Ser Tyr Gln Pro Met
20 25 30

gag aaa gtg ttt ccg tac gac aag tac gaa ggc atc aag atc cac gat 144
Glu Lys Val Phe Pro Tyr Asp Lys Tyr Glu Gly Ile Lys Ile His Asp
35 40 45

tgg gat aaa tgg gaa gac ccc ttc cgc ctg acc atg gac gcc tac tgg 192
Trp Asp Lys Trp Glu Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
50 55 60

aaa tat cag ggc gag aag gaa aaa aag ctt tac gcc gtc atc gac gct 240
Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
65 70 75 80

ttc gcg cag aac aac ggg cag ttg agc att tcc gac gcg cga tat gtc 288
Phe Ala Gln Asn Asn Gly Gln Leu Ser Ile Ser Asp Ala Arg Tyr Val
85 90 95

aac gca ctc aag gtg ttt atc cag ggt gtg aca ccg ttg gag tat atg 336
Asn Ala Leu Lys Val Phe Ile Gln Gly Val Thr Pro Leu Glu Tyr Met

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100	105	110	
gca cac cga ggt ttt gcc cac att ggt cgg cat ttt acg ggt gaa ggg Ala His Arg Gly Phe Ala His Ile Gly Arg His Phe Thr Gly Glu Gly	115	120	384
125			
gca cgt gtt gct tgc cag atg cag tcc atc gac gag ctg cgt cac ttc Ala Arg Val Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Phe	130	135	432
140			
cag acc gaa atg cat gct ctc tcg cac tac aac aag tat ttt aac ggt Gln Thr Glu Met His Ala Leu Ser His Tyr Asn Lys Tyr Phe Asn Gly	145	150	480
155			
160			
ctg cac aac tcc atc cat tgg tac gac cgg gtt tgg tat ttg tcg gtg Leu His Asn Ser Ile His Trp Tyr Asp Arg Val Trp Tyr Leu Ser Val	165	170	528
175			
ccc aag tca ttt ttt gaa gac gcg gcc acc ggt gga ccg ttc gag ttt Pro Lys Ser Phe Phe Glu Asp Ala Ala Thr Gly Gly Pro Phe Glu Phe	180	185	576
190			
ctt acc gcg gtg agc ttt tcg ttc gaa tat gtg ttg acc aac ctg ctg Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu	195	200	624
205			
ttt gtc ccc ttc atg tcg ggt gct gct tac aac ggg gac atg tct acg Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr	210	215	672
220			
gtc act ttc ggt ttt tcg gcg caa agt gac gaa tcg cgc cac atg aca Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr	225	230	720
240			
ctc ggc atc gaa tgc atc aag ttc atg cta gaa cag gat ccg gac aac Leu Gly Ile Glu Cys Ile Lys Phe Met Leu Glu Gln Asp Pro Asp Asn	245	250	768
255			
gtg ccc atc gtg cag cgc tgg atc gac aag tgg ttc tgg cgc ggc tat Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr	260	265	816
270			
cgg ctg ttg agc atc gtg gcc atg atg cag gac tac atg ctg ccc aac Arg Leu Leu Ser Ile Val Ala Met Met Gln Asp Tyr Met Leu Pro Asn	275	280	864
285			
cgg gtg atg agc tgg cgc gag agc tgg gag atg tac gtc gag cag aac Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Val Glu Gln Asn	290	295	912
300			
ggc ggc gcg ctg ttc aag gat ctt gcg cgt tat ggc atc cgc aag ccc Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Ile Arg Lys Pro	305	310	960
315			
320			
aag ggc tgg gac cag gct tgc gaa ggc aag gac cac atc agc cat cag Lys Gly Trp Asp Gln Ala Cys Glu Gly Lys Asp His Ile Ser His Gln	325	330	1008
335			
acc ttc gcc gta ttc tat aac tat aac gcc gcg gcc ccc atc cac acc Thr Phe Ala Val Phe Tyr Asn Tyr Asn Ala Ala Pro Ile His Thr	340	345	1056
350			
tgg gtt ccc aca aaa gaa gaa atg gga tgg ctg tcg gag aag tac ccc Trp Val Pro Thr Lys Glu Met Gly Trp Leu Ser Glu Lys Tyr Pro	355	360	1104
365			
gag acg ttc gac aag tat tac cgt ccg cgt tgg gac tac tgg cgc gag Glu Thr Phe Asp Lys Tyr Tyr Arg Pro Arg Trp Asp Tyr Trp Arg Glu	370	375	1152
380			
cag gcc aag ggc aac cgt ttc tac aac aag acg ctg ccg atg ctc Gln Ala Ala Lys Gly Asn Arg Phe Tyr Asn Lys Thr Leu Pro Met Leu	385	390	1200
395			
400			
tgc act acc tgc cag att ccg atg ata ttc acc gag cct ggc gac gca Cys Thr Thr Cys Gln Ile Pro Met Ile Phe Thr Glu Pro Gly Asp Ala			1248

405

410

415

acc aag atc tgc tat cgc gag tcg gcc tac ctc ggc gac aag tat cac Thr Lys Ile Cys Tyr Arg Glu Ser Ala Tyr Leu Gly Asp Lys Tyr His	1296
420 425 430	
ttc tgc agc gac cac tgc aag gag att ttt gac aac gaa ccc gaa aag Phe Cys Ser Asp His Cys Lys Glu Ile Phe Asp Asn Glu Pro Glu Lys	1344
435 440 445	
ttc gtg cag tca tgg ctt ccg ccg cag caa gtg tat caa gga aac tgt Phe Val Gln Ser Trp Leu Pro Pro Gln Gln Val Tyr Gln Gly Asn Cys	1392
450 455 460	
ttc aag ccg gat gcc gat ccg acc aag gag ggt ttt gat ccc ttg atg Phe Lys Pro Asp Ala Asp Pro Thr Lys Glu Gly Phe Asp Pro Leu Met	1440
465 470 475 480	
gcc ttg ctc gac tac tac aac ctg aat gta ggc ccg gac aac ttc gat Ala Leu Leu Asp Tyr Tyr Asn Leu Asn Val Gly Arg Asp Asn Phe Asp	1488
485 490 495	
ttc gag gga tcg gaa gac caa aag aac ttt gct gcc tgg cgt gga gag Phe Glu Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Glu	1536
500 505 510	
gtc ttg caa gga gaa gcc aaa tga Val Leu Gln Gly Glu Ala Lys	1560
515	

<210> 28
<211> 519
<212> PRT
<213> Burkholderia cepacia

<400> 28

Met Asp Thr Ser Val Gln Lys Lys Lys Leu Gly Leu Lys Asn Arg Tyr	
1 5 10 15	
Ala Ala Met Thr Arg Gly Leu Gly Trp Gln Thr Ser Tyr Gln Pro Met	
20 25 30	
Glu Lys Val Phe Pro Tyr Asp Lys Tyr Glu Gly Ile Lys Ile His Asp	
35 40 45	
Trp Asp Lys Trp Glu Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp	
50 55 60	
Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala	
65 70 75 80	
Phe Ala Gln Asn Asn Gly Gln Leu Ser Ile Ser Asp Ala Arg Tyr Val	
85 90 95	
Asn Ala Leu Lys Val Phe Ile Gln Gly Val Thr Pro Leu Glu Tyr Met	
100 105 110	
Ala His Arg Gly Phe Ala His Ile Gly Arg His Phe Thr Gly Glu Gly	
115 120 125	
Ala Arg Val Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Phe	
130 135 140	
Gln Thr Glu Met His Ala Leu Ser His Tyr Asn Lys Tyr Phe Asn Gly	
145 150 155 160	
Leu His Asn Ser Ile His Trp Tyr Asp Arg Val Trp Tyr Leu Ser Val	
165 170 175	
Pro Lys Ser Phe Phe Glu Asp Ala Ala Thr Gly Gly Pro Phe Glu Phe	
180 185 190	
Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu	
195 200 205	

Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
 210 215 220
 Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
 225 230 235 240
 Leu Gly Ile Glu Cys Ile Lys Phe Met Leu Glu Gln Asp Pro Asp Asn
 245 250 255
 Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
 260 265 270
 Arg Leu Leu Ser Ile Val Ala Met Met Gln Asp Tyr Met Leu Pro Asn
 275 280 285
 Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Val Glu Gln Asn
 290 295 300
 Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Lys Pro
 305 310 315 320
 Lys Gly Trp Asp Gln Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
 325 330 335
 Thr Phe Ala Val Phe Tyr Asn Tyr Asn Ala Ala Pro Ile His Thr
 340 345 350
 Trp Val Pro Thr Lys Glu Glu Met Gly Trp Leu Ser Glu Lys Tyr Pro
 355 360 365
 Glu Thr Phe Asp Lys Tyr Tyr Arg Pro Arg Trp Asp Tyr Trp Arg Glu
 370 375 380
 Gln Ala Ala Lys Gly Asn Arg Phe Tyr Asn Lys Thr Leu Pro Met Leu
 385 390 395 400
 Cys Thr Thr Cys Gln Ile Pro Met Ile Phe Thr Glu Pro Gly Asp Ala
 405 410 415
 Thr Lys Ile Cys Tyr Arg Glu Ser Ala Tyr Leu Gly Asp Lys Tyr His
 420 425 430
 Phe Cys Ser Asp His Cys Lys Glu Ile Phe Asp Asn Glu Pro Glu Lys
 435 440 445
 Phe Val Gln Ser Trp Leu Pro Pro Gln Gln Val Tyr Gln Gly Asn Cys
 450 455 460
 Phe Lys Pro Asp Ala Asp Pro Thr Lys Glu Gly Phe Asp Pro Leu Met
 465 470 475 480
 Ala Leu Leu Asp Tyr Tyr Asn Leu Asn Val Gly Arg Asp Asn Phe Asp
 485 490 495
 Phe Glu Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Glu
 500 505 510
 Val Leu Gln Gly Glu Ala Lys
 515

<210> 29
 <211> 996
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (1)..(996)

<400> 29
 atg acc atc gat ttg aag acg cgg gaa atc aaa cca ctg cgt cac acc
 Met Thr Ile Asp Leu Lys Thr Arg Glu Ile Lys Pro Leu Arg His Thr
 1 5 10 15

tac acg cac gtg gct caa tac atc ggg gcc gat aaa gcc gct tcg cgc Tyr Thr His Val Ala Gln Tyr Ile Gly Ala Asp Lys Ala Ala Ser Arg 20 25 30	96
tat cag gaa ggc act gta ggt gct caa ccc gca gcg aat ttt cat tac Tyr Gln Glu Gly Thr Val Gly Ala Gln Pro Ala Ala Asn Phe His Tyr 35 40 45	144
cgg ccc acg tgg gat ccc gag cat gaa ctg ttc gac acg tcg cgt acc Arg Pro Thr Trp Asp Pro Glu His Glu Leu Phe Asp Thr Ser Arg Thr 50 55 60	192
gcg att caa atg aag gac tgg tat gcg ctg aaa gac ccg cgt cag ttc Ala Ile Gln Met Lys Asp Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe 65 70 75 80	240
tac tac gcg tcg tgg acg atg acc cga gcg cgg cag caa gac gcg atg Tyr Tyr Ala Ser Trp Thr Met Thr Arg Ala Arg Gln Gln Asp Ala Met 85 90 95	288
gaa tcc aac ttc gag ttt gtc gag tcg cgc ggc atg atc gat ctc gtt Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Gly Met Ile Asp Leu Val 100 105 110	336
tcc gat gag gtt cga caa cgg gcg ctt tcc gtt ctc gtg cct ttg cgt Ser Asp Glu Val Arg Gln Arg Ala Leu Ser Val Leu Val Pro Leu Arg 115 120 125	384
cac gcg gcc tgg ggc gcg aac atg aac aac tcc cag atc tgt gcc cta His Ala Ala Trp Gly Ala Asn Met Asn Asn Ser Gln Ile Cys Ala Leu 130 135 140	432
ggt tat ggc acg acc ttc act gcg ccg gct atg ttc cac gca atg gac Gly Tyr Gly Thr Phe Thr Ala Pro Ala Met Phe His Ala Met Asp 145 150 155 160	480
aat ctg ggt gta gcg cag tat ctc aca cga ctg gcg ctg gta atg tct Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Val Met Ser 165 170 175	528
gga ccc gat ctt ctt gac gaa gcc aag caa gcc tgg atg acg agt ccc Gly Pro Asp Leu Leu Asp Glu Ala Lys Gln Ala Trp Met Thr Ser Pro 180 185 190	576
gat tgg caa ccg ttg cgt cgt tat gtg gaa aac act ctg gtg ctg caa Asp Trp Gln Pro Leu Arg Arg Tyr Val Glu Asn Thr Leu Val Leu Gln 195 200 205	624
gat ccg gtg gaa ctg ttc atc gcc caa aat ctg gcg ctc gac ggt ctt Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu 210 215 220	672
ctt tat ccc atg atc tac ggc gct ttc gtc gac gat tac atc gca ctc Leu Tyr Pro Met Ile Tyr Gly Ala Phe Val Asp Asp Tyr Ile Ala Leu 225 230 235 240	720
aac ggt ggt agc gca gtg gca atg cta acc act ttc atg ccc gag tgg Asn Gly Gly Ser Ala Val Ala Met Leu Thr Thr Phe Met Pro Glu Trp 245 250 255	768
cat gac gaa tcc agt cgc tgg gtc gat gcg gta gta aag acc atg gcg His Asp Glu Ser Ser Arg Trp Val Asp Ala Val Val Lys Thr Met Ala 260 265 270	816
acg gaa tcg gag gat aac aaa gcg ctg ctc att cac tgg ttg cgt acc Thr Glu Ser Glu Asp Asn Lys Ala Leu Leu Ile His Trp Leu Arg Thr 275 280 285	864
tgg gaa gat cag gcg gcg tca gcg ttg ttg cct gtc gct gaa atg gct Trp Glu Asp Gln Ala Ala Ser Ala Leu Leu Pro Val Ala Glu Met Ala 290 295 300	912
ttg gcg gaa aac ggc cac gac gcc ttg gaa gaa gta agg cag caa ctt Leu Ala Glu Asn Gly His Asp Ala Leu Glu Glu Val Arg Gln Gln Leu 305 310 315 320	960

cgt gcc cgc gtt gcg aag gcc ggg att gtt ctg taa	996
Arg Ala Arg Val Ala Lys Ala Gly Ile Val Leu	
325	330
<210> 30	
<211> 331	
<212> PRT	
<213> Burkholderia cepacia	
<400> 30	
Met Thr Ile Asp Leu Lys Thr Arg Glu Ile Lys Pro Leu Arg His Thr	
1	5
10	15
Tyr Thr His Val Ala Gln Tyr Ile Gly Ala Asp Lys Ala Ala Ser Arg	
20	25
30	
Tyr Gln Glu Gly Thr Val Gly Ala Gln Pro Ala Ala Asn Phe His Tyr	
35	40
45	
Arg Pro Thr Trp Asp Pro Glu His Glu Leu Phe Asp Thr Ser Arg Thr	
50	55
60	
Ala Ile Gln Met Lys Asp Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe	
65	70
75	80
Tyr Tyr Ala Ser Trp Thr Met Thr Arg Ala Arg Gln Gln Asp Ala Met	
85	90
95	
Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Gly Met Ile Asp Leu Val	
100	105
110	
Ser Asp Glu Val Arg Gln Arg Ala Leu Ser Val Leu Val Pro Leu Arg	
115	120
125	
His Ala Ala Trp Gly Ala Asn Met Asn Asn Ser Gln Ile Cys Ala Leu	
130	135
140	
Gly Tyr Gly Thr Thr Phe Thr Ala Pro Ala Met Phe His Ala Met Asp	
145	150
155	160
Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Val Met Ser	
165	170
175	
Gly Pro Asp Leu Leu Asp Glu Ala Lys Gln Ala Trp Met Thr Ser Pro	
180	185
190	
Asp Trp Gln Pro Leu Arg Arg Tyr Val Glu Asn Thr Leu Val Leu Gln	
195	200
205	
Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu	
210	215
220	
Leu Tyr Pro Met Ile Tyr Gly Ala Phe Val Asp Asp Tyr Ile Ala Leu	
225	230
235	240
Asn Gly Gly Ser Ala Val Ala Met Leu Thr Thr Phe Met Pro Glu Trp	
245	250
255	
His Asp Glu Ser Ser Arg Trp Val Asp Ala Val Val Lys Thr Met Ala	
260	265
270	
Thr Glu Ser Glu Asp Asn Lys Ala Leu Leu Ile His Trp Leu Arg Thr	
275	280
285	
Trp Glu Asp Gln Ala Ala Ser Ala Leu Leu Pro Val Ala Glu Met Ala	
290	295
300	
Leu Ala Glu Asn Gly His Asp Ala Leu Glu Val Arg Gln Gln Leu	
305	310
315	320
Arg Ala Arg Val Ala Lys Ala Gly Ile Val Leu	
325	330

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<210> 31
<211> 357
<212> DNA
<213> Burkholderia cepacia

<220>
<221> CDS
<222> (1)..(357)

<400> 31
atg agc gtt gtt gcc ctc aaa ccc tac aag ttc ccg gca cga gac gcg      48
Met Ser Val Val Ala Leu Lys Pro Tyr Lys Phe Pro Ala Arg Asp Ala
1           5           10          15

cgc gaa aac ttt ccg gcg ccg ttg ctg ttt atc ggc tgg gaa gac cat      96
Arg Glu Asn Phe Pro Ala Pro Leu Leu Phe Ile Gly Trp Glu Asp His
20          25          30

ctg ttg ttt gcg gca cct gtt gcc ttg ccc ctg ccg tcg gac acg ttg      144
Leu Leu Phe Ala Ala Pro Val Ala Leu Pro Leu Pro Ser Asp Thr Leu
35          40          45

ttc ggt gcg ctg tgc acc cag gtg ttg ccc ggc act tat ggc tat cac      192
Phe Gly Ala Leu Cys Thr Gln Val Leu Pro Gly Thr Tyr Gly Tyr His
50          55          60

ccc gat ttc tca aag atc gac tgg agc cag gtg cag tgg ttt aag tcc      240
Pro Asp Phe Ser Lys Ile Asp Trp Ser Gln Val Gln Trp Phe Lys Ser
65          70          75          80

ggc cag ccg tgg cat ccc gac ccg gcg aag tcg ctg gct gaa aac ggt      288
Gly Gln Pro Trp His Pro Asp Pro Ala Lys Ser Leu Ala Glu Asn Gly
85          90          95

ctg acg cac aaa gac gtg atc cgc ttt cgc acg cct ggc ttg aac ggt      336
Leu Thr His Lys Asp Val Ile Arg Phe Arg Thr Pro Gly Leu Asn Gly
100         105         110

ctg agc ggt tcc tgc aat tga                                         357
Leu Ser Gly Ser Cys Asn
115

<210> 32
<211> 118
<212> PRT
<213> Burkholderia cepacia

<400> 32
Met Ser Val Val Ala Leu Lys Pro Tyr Lys Phe Pro Ala Arg Asp Ala
1           5           10          15

Arg Glu Asn Phe Pro Ala Pro Leu Leu Phe Ile Gly Trp Glu Asp His
20          25          30

Leu Leu Phe Ala Ala Pro Val Ala Leu Pro Leu Pro Ser Asp Thr Leu
35          40          45

Phe Gly Ala Leu Cys Thr Gln Val Leu Pro Gly Thr Tyr Gly Tyr His
50          55          60

Pro Asp Phe Ser Lys Ile Asp Trp Ser Gln Val Gln Trp Phe Lys Ser
65          70          75          80

Gly Gln Pro Trp His Pro Asp Pro Ala Lys Ser Leu Ala Glu Asn Gly
85          90          95

Leu Thr His Lys Asp Val Ile Arg Phe Arg Thr Pro Gly Leu Asn Gly
100         105         110

Leu Ser Gly Ser Cys Asn
115

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<210> 33
<211> 1143
<212> DNA
<213> Bacillus stearothermophilus

<220>
<221> CDS
<222> (1)..(1143)

<400> 33
atg gaa aaa aat aaa atg tta ata gaa gaa aag ttg gac act gct gct      48
Met Glu Lys Asn Lys Met Leu Ile Glu Glu Lys Leu Asp Thr Ala Ala
1          5           10          15

ctt ctt gct aag gcg gag gaa ata ggc cg att gct gag gaa gag gcg      96
Leu Leu Ala Lys Ala Glu Glu Ile Gly Arg Ile Ala Glu Glu Glu Ala
20         25           30

gg gaa gcg gac cgc aat gcc tgt ttc tcc gac cg gt gct agg gcc      144
Gly Glu Ala Asp Arg Asn Ala Cys Phe Ser Asp Arg Val Ala Arg Ala
35         40           45

att aaa gaa gct gga ttc cac aag ctc atg cgt ccc aag cag tac gga      192
Ile Lys Glu Ala Gly Phe His Lys Leu Met Arg Pro Lys Gln Tyr Gly
50         55           60

gga ctg caa gta gac ttg cga act tac ggg gag att gtc cg aca gt      240
Gly Leu Gln Val Asp Leu Arg Thr Tyr Gly Glu Ile Val Arg Thr Val
65         70           75           80

gcc cgg tac agt gtt gcc gca gga tgg ctg acc tat ttt tat tcc at      288
Ala Arg Tyr Ser Val Ala Ala Gly Trp Leu Thr Tyr Phe Tyr Ser Met
85         90           95

cat gag gtt tgg gct gca tat ctg cct cca aaa gg aga gaa gaa att      336
His Glu Val Trp Ala Ala Tyr Leu Pro Pro Lys Gly Arg Glu Glu Ile
100        105          110

ttt gga caa gga ggg ctg ttg gca gac gtc gtt gcc cct gtt gg cg      384
Phe Gly Gln Gly Leu Leu Ala Asp Val Val Ala Pro Val Gly Arg
115        120          125

gtg gag aag gac ggg gac gg tac cgt ctc tat ggg cag tgg aac tt      432
Val Glu Lys Asp Gly Asp Gly Tyr Arg Leu Tyr Gly Gln Trp Asn Phe
130        135          140

tgt agc ggt gtc ctc cat agt gac tgg atc gga ctt gg gc atg at      480
Cys Ser Gly Val Leu His Ser Asp Trp Ile Gly Leu Gly Ala Met Met
145        150          155          160

gag ctg cct gac gg aat agt cct gag tac tgt ttg tta gtg ctg cct      528
Glu Leu Pro Asp Gly Asn Ser Pro Glu Tyr Cys Leu Leu Val Leu Pro
165        170          175

aag tcg gat gtc cag atc gta gaa aat tgg gat acc atg gg ctc cg      576
Lys Ser Asp Val Gln Ile Val Glu Asn Trp Asp Thr Met Gly Leu Arg
180        185          190

gct tcg gga agc aac ggg gta tta gtt gaa ggt gct tat gtt cca tta      624
Ala Ser Gly Ser Asn Gly Val Leu Val Glu Gly Ala Tyr Val Pro Leu
195        200          205

cac cg atc tt ccg gct gg cg gt atg gct cat ccg ctt tt cc tt      672
His Arg Ile Phe Pro Ala Gly Arg Val Met Ala His Pro Leu Phe Leu
210        215          220

ctt ggg tt cct tta gta tct tta gg gc gg c gac gaa cga tt g gt tca      720
Leu Gly Phe Pro Leu Val Ser Leu Gly Gly Asp Glu Arg Leu Val Ser
225        230          235          240

ctt tt cca gaa cg act gag aag cg att cgt gtc tt cca aa gg gg      768
Leu Phe Gln Glu Arg Thr Glu Lys Arg Ile Arg Val Phe Lys Gly Gly
245        250          255

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gct aaa gaa aag gat tct gcc gct agc cag cgg ctg tta gcc gag atg Ala Lys Glu Lys Asp Ser Ala Ala Ser Gln Arg Leu Leu Ala Glu Met 260 265 270	816
aaa aca gaa tta aat gca atg gaa ggc att gtg gaa caa tat atc cgc Lys Thr Glu Leu Asn Ala Met Glu Gly Ile Val Glu Gln Tyr Ile Arg 275 280 285	864
cag ctt gag gct tgc caa aaa gaa gga aag acg gtg atg aac gat atg Gln Leu Glu Ala Cys Gln Lys Glu Gly Lys Thr Val Met Asn Asp Met 290 295 300	912
gag cga gag cag cta ttc gca tgg cgt gga tat gtg gca aaa gcg tcc Glu Arg Glu Gln Leu Phe Ala Trp Arg Gly Tyr Val Ala Lys Ala Ser 305 310 315 320	960
gcc aat att gcc gtc aga aca ctg tta act ctt gga ggc aat tcg atc Ala Asn Ile Ala Val Arg Thr Leu Leu Thr Leu Gly Gly Asn Ser Ile 325 330 335	1008
ttt aaa ggc gat ccg gta gaa ctg ttc aca aga gat ttg cta gcg gtg Phe Lys Gly Asp Pro Val Glu Leu Phe Thr Arg Asp Leu Leu Ala Val 340 345 350	1056
gcc gca cat cct aac tcc ctg tgg gag gat gcg atg gct gca tat gga Ala Ala His Pro Asn Ser Leu Trp Glu Asp Ala Met Ala Ala Tyr Gly 355 360 365	1104
aga acg ata ttc ggg ctg cca ggg gac cca gtc tgg taa Arg Thr Ile Phe Gly Leu Pro Gly Asp Pro Val Trp 370 375 380	1143
<210> 34	
<211> 380	
<212> PRT	
<213> <i>Bacillus stearothermophilus</i>	
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Ile Lys Glu Ala Gly Phe His Lys Leu Met Arg Pro Lys Gln Tyr Gly 50 55 60	
Gly Leu Gln Val Asp Leu Arg Thr Tyr Gly Glu Ile Val Arg Thr Val 65 70 75 80	
Ala Arg Tyr Ser Val Ala Ala Gly Trp Leu Thr Tyr Phe Tyr Ser Met 85 90 95	
His Glu Val Trp Ala Ala Tyr Leu Pro Pro Lys Gly Arg Glu Glu Ile 100 105 110	
Phe Gly Gln Gly Gly Leu Leu Ala Asp Val Val Ala Pro Val Gly Arg 115 120 125	
Val Glu Lys Asp Gly Asp Gly Tyr Arg Leu Tyr Gly Gln Trp Asn Phe 130 135 140	
Cys Ser Gly Val Leu His Ser Asp Trp Ile Gly Leu Gly Ala Met Met 145 150 155 160	
Glu Leu Pro Asp Gly Asn Ser Pro Glu Tyr Cys Leu Leu Val Leu Pro 165 170 175	
Lys Ser Asp Val Gln Ile Val Glu Asn Trp Asp Thr Met Gly Leu Arg 180 185 190	

Ala Ser Gly Ser Asn Gly Val Leu Val Glu Gly Ala Tyr Val Pro Leu
 195 200 205
 His Arg Ile Phe Pro Ala Gly Arg Val Met Ala His Pro Leu Phe Leu
 210 215 220
 Leu Gly Phe Pro Leu Val Ser Leu Gly Gly Asp Glu Arg Leu Val Ser
 225 230 235 240
 Leu Phe Gln Glu Arg Thr Glu Lys Arg Ile Arg Val Phe Lys Gly Gly
 245 250 255
 Ala Lys Glu Lys Asp Ser Ala Ala Ser Gln Arg Leu Leu Ala Glu Met
 260 265 270
 Lys Thr Glu Leu Asn Ala Met Glu Gly Ile Val Glu Gln Tyr Ile Arg
 275 280 285
 Gln Leu Glu Ala Cys Gln Lys Glu Gly Lys Thr Val Met Asn Asp Met
 290 295 300
 Glu Arg Glu Gln Leu Phe Ala Trp Arg Gly Tyr Val Ala Lys Ala Ser
 305 310 315 320
 Ala Asn Ile Ala Val Arg Thr Leu Leu Thr Leu Gly Gly Asn Ser Ile
 325 330 335
 Phe Lys Gly Asp Pro Val Glu Leu Phe Thr Arg Asp Leu Leu Ala Val
 340 345 350
 Ala Ala His Pro Asn Ser Leu Trp Glu Asp Ala Met Ala Ala Tyr Gly
 355 360 365
 Arg Thr Ile Phe Gly Leu Pro Gly Asp Pro Val Trp
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<220>
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 tca ttc gcg ttt cct caa ccg aaa cct ctc aga tct ccc aaa ttc gcc 96
 Ser Phe Ala Phe Pro Gln Pro Lys Pro Leu Arg Ser Pro Lys Phe Ala
 20 25 30
 atg gct tcc acc att gga tcc gct aca acg aag gtt gaa agc acc aaa 144
 Met Ala Ser Thr Ile Gly Ser Ala Thr Thr Lys Val Glu Ser Thr Lys
 35 40 45
 aag ccc ttt acc cct cca agg gag gtt cac caa cag gtg cta cac tca 192
 Lys Pro Phe Thr Pro Arg Glu Val His Gln Gln Val Leu His Ser
 50 55 60
 atg ccg cca caa aag atc gaa atc ttc aaa tcc atg gag ggt tgg gcc 240
 Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Met Glu Gly Trp Ala
 65 70 75 80
 gaa aat aac ata ttg gtt cac cta aag cct gtc gaa aaa tgc tgg caa 288
 Glu Asn Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln
 85 90 95
 gca cag gat ttc cta cca gat ccc gca tct gac gga ttt atg gaa caa 336
 Ala Gln Asp Phe Leu Pro Asp Pro Ala Ser Asp Gly Phe Met Glu Gln
 100 105 110

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Ser Phe Ala Phe Pro Gln Pro Lys Pro Leu Arg Ser Pro Lys Phe Ala
 20 25 30

Met Ala Ser Thr Ile Gly Ser Ala Thr Thr Lys Val Glu Ser Thr Lys
 35 40 45

Lys Pro Phe Thr Pro Pro Arg Glu Val His Gln Gln Val Leu His Ser
 50 55 60

Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Met Glu Gly Trp Ala
 65 70 75 80

Glu Asn Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln
 85 90 95

Ala Gln Asp Phe Leu Pro Asp Pro Ala Ser Asp Gly Phe Met Glu Gln
 100 105 110

Val Glu Glu Leu Arg Ala Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
 115 120 125

Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
 130 135 140

Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
 145 150 155 160

Thr Leu Leu Leu Gly Leu Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
 165 170 175

Asn Arg His Gly Asp Leu Leu His Gln Tyr Leu Tyr Leu Ser Gly Arg
 180 185 190

Val Asp Met Arg Gln Ile Gln Lys Thr Ile Gln Tyr Leu Ile Gly Ser
 195 200 205

Gly Met Asp Pro Arg Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr
 210 215 220

Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
 225 230 235 240

Arg His Ala Lys Glu His Gly Asp Val Lys Leu Ala Gln Met Cys Gly
 245 250 255

Ile Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
 260 265 270

Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Leu Ala Phe
 275 280 285

Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Tyr
 290 295 300

Asp Gly Arg Asp Asp Asn Leu Phe Glu Asn Phe Ser Ala Val Ala Gln
 305 310 315 320

Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe
 325 330 335

Leu Val Gly Arg Trp Lys Val Ala Asp Leu Thr Gly Leu Ser Gly Glu
 340 345 350

Gly Arg Lys Ala Gln Asp Tyr Val Cys Gly Leu Ala Pro Arg Ile Arg
 355 360 365

Arg Leu Glu Glu Arg Asn Ser Ala Arg Ala Lys Glu Ser Val Asn Val
 370 375 380

Pro Phe Ser Trp Ile Phe Asp Arg Glu Val Lys Leu

